stack; Lectin; Manganese;

7

us-10-092-750-32.rup

```
SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=C57BL/60; TISSUE=Adipose tissue;

MEDININ=25394683; PubMed=1246685; DOI=10.1038/nature01266;

RA

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA

Rajak K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Ra Baldarelli R., Fill D.P., Bult C., Hume D.A., Guackenbush J.,

RA Barke J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Caraba C., Godzik A., Frazer K.S.,

RA Gasterland T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Kanai A., Kawaji H., Kawasawa Y., Kadzierski R.N., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kadzierski R.N., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magashima T., Numata K., Okido T., Pavan W.J., Pertae G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Ravasi T., Rechnaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

RA Verardo R., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yangur M., Yang I., Yang L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIT2_MOUSE STANDARD; PRT; 570 AA.

QERBS; QTT2ES; QBELST; Q92KE; Q99MEI;

QERBS; QTT2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
01-0CT-2004 (Rel. 45, Last sequence and updates 2 (EC 2.4.1.41)
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (UDP-0CT-2004)
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence and updates 2) (Contains:
01-0CT-2004 (Rel. 45, Last sequence 2) (Rel. 41)
01-0CT-2004 (Rel. 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 128.5; DB 1; Length 558; 55.6%; Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 CGGSLEIVPCSRVGHVFRKRHPYNPPEGNALTYIRNTKRTAEVWM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVSLA--RNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUBECOlon adenocarcinoma,
Miyahara N., Kanoh A., Irimura T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2FE9B0CAD13FC8AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Catalytic subdomain A. Catalytic subdomain B.
                                                                                                                                                                                                                                                                                                                                                                                                                               Ricin. B-type lectin. By similarity. By similarity. By similarity. By similarity.
                                                                                                                                                                                                                                                                            Signal-anchor for tr
protein (Potential)
Lumenal (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.9e-09;
6; Mismatches 11
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00535; Glycos_transf_2; 1.
Pfam; PF00652; Ricin_B_lectin; 2.
SWART; SMO0458; RICIN_F. 1.
PROSITE; PSS0231; RICIN_B_LECTIN; 1.
Calcium; Glycosyltransferase; Golgi stack; Signal-anchor; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 55.6
25; Conservative
                                                                                                                                                                                                                                                                                                                                        555
505
506
506
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506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                          Signal-anchor; T
DOMAIN
TRANSMEM 7
                                                                                                                                                                                                                                                                                                                                                                       122
286
4428
444
530
                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                           DOMAIN
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GLT2 MOUSE
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          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissub SPECIFICITY: In the CNS, it is predominantly expressed in several distinct hypothalamic, thalamic and amygdaloid nuclei. The most abundant level of expression is in the paraventricular, ventromedial and arcuate nuclei of the hypothalamus, the anterodorsal and parafascicular nuclei of the thalamus and central, basomedial and medial nuclei of the amygdala. Also expressed in cerebral cortex, lateral septum, habenula and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GTI motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNAc-T motif), which is probably involved in catalytic reaction and UDP-Gal binding (By similarity).
DOMAIN: The rich B-type lectin domain binds to GalNAc and contributes to the glycopeptide specificity (By similarity).
SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                       01-0cT-2004 (Rel. 45, Created)
01-0cT-2004 (Rel. 45, Last sequence update)
01-0cT-2004 (Rel. 45, Last sequence update)
Putative polypeptide N-acety-galactosaminyltransferase-like protein 16EC 2.4.1.41) (Protein-UDP acety-lgalactosaminyltransferase-like protein 1) (UDP-GalNAc:polypeptide N-acety-lgalactosaminyltransferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1) (Polypeptide GalNAc transferase-like protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson P.A., Sutcliffe J.G., Thomas B.A., Parelylgalactosaminyltransferase mRNA exhibits predominant expression in the hypothalamus, thalamus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Expr. Patterns 1:95-99 (2002).

-!- FUNCTION: May catalyze the initial reaction in O-linked oligosaccharide biosynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the protein receptor (By similarity).

-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide UDP + N-acetyl-D-galactosaminy1-polypeptide.

-!- COPACTOR: Manganese and calcium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 ricin B-type lectin domain.
-!- CAUTION: Was originally (Ref.2) termed Galnt10/pp-GaNTase 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
Hashimoto K.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                      558 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB045325; BAA97985.1; -.
MGD; MGI:1947754; Galntll.
InterPro; IPR001173; Glyco_trans_2.
InterPro; IPR008997; RichnB_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amygdala of mouse forebrain.";
Gene Expr. Patterns 1:95-99(2002)
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Name=Galntl1;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15018805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hippocampus.
DOMAIN: There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                           GTL1 MOUSE
Q9JJ61;
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5

Gaps

٠. س

11; Indels

셤 OSEPPE SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN-C57BL/6, and Czech II; TISSUE=Brain, and Breast tumor;

XX MEDINE=2238825; PubMed=12477932; DOT=10.1073/pnas.24263899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

XA Altschul S.F., Zeeberg B. B., Buetow K.H., Schmen C.M., Schuler G.D.,

Antschul S.F., Zeeberg B. B., Buetow K.H., Schmen C.M., Haibar N. R.,

Antschul S.F., Zeeberg B. B., Buetow K.H., Schmefr C.F., Bhar N. R.,

Antschul S.F., Zeeberg B. B., Buetow K.H., Schmefr C.F., Bhar N. R.,

Antschul S.F., Zeeberg B. B., Boratow G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Stapleron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Antlalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Antiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Antiting M., Madan A., Young A.C., Schmutz J., Dickson M.C.,

Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,

Roderation and initial analysis of more than 15,000 full-length human Name=2; Sequence=VSP 011201;
Isold=Q6PB93-2; Sequence=VSP 011201;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
ISSUE SPECIFICITY: Widely expressed at high level.
DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GTI motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called GB1/GB1NAc-T motif), which is probably involved in catalytic reaction and UDP-GB1 binding (By similarity).
DOMAIN: The ricin B-type lectin domain binds to GB1NAc and contributes to the glycosptide specificity (By similarity).
SIMILARITY: Belongs to the glycosyltransferase family 2. GB1NAc-T -!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide = UDP + N-acetyl-D-galactosaminyl-polypeptide.
-!- COFACTOR: Manganese and calcium (By similarity)
-!- PATHWAY: Glycosylation
-!- SUBCELIULAR LOCATION: Type II membrane protein. Golgi; resides preferentially in the trans and medial parts of the Golgi stack. A Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komo H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sakai K., Sakai K., Shihata K., S acetylgalactosaminyltranseerisciorms in murine tissues determined by real-time PCR: a new view of a large family.";

Glycobiology 13:549-557(2003)

-!- FUNCTION: Catalyzes the initial reaction in O-linked oligosaccharide biosynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the protein receptor. Has a broad spectrum of substrates for peptides such as EA2, MucSAC, Mucla, Muclb. Probably involved in O-linked glycosylation of the immunoglobulin A1 (IGA1) hinge region (By PubMed=12651884; DOI=10.1093/glycob/cwg062; Young W.W. Jr., Holcomb D.R., Ten Hagen K.G., Tabak L.A.; "Expression of UDP-GalNAc:polypeptide Nroc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) Event=Alternative splicing; Named isoforms=2; IsoId=Q6PB93-1; Sequence=Displayed; secreted form also exists. ALTERNATIVE PRODUCTS: and mouse cDNA sequences." IISSUE SPECIFICITY

```
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin B-type lectin.
Not glycosylated (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
MRRRSRMLLCFALLWVLGIAYYMYSGGGSALAAGGGCAGRK
                                                                                                                                                                                                                                                                                                                                                R HSSP, P26514; IXMM.

R MGD; MGI:894694; Galnt2.

R MGD; MGI:894694; Galnt2.

R InterPro; IPR000173; Glyco trans_2.

R InterPro; IPR000977; Ricin B lectin.

DR PROSTS; Glycos trans[2]: 1.

DR Fam; PF00652; Ricin B lectin, 2.

DR PROSTS; P850231; RICIN B LECTIN; 1.

DR PROSTS; P850231; RICIN B LECTIN; 1.

RM Alternative splicing; Calcium; Glycosyltransferase; Golgi stack; KW lectin; Manganese; Signal-anchor; Transferase; Transmembrane.

FT PROPEP 1 50 Removed in soluble polypeptide N-initarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide N-
acetylgalactosaminyltransferase 2,
acetylgalactosaminyltransferase 2,
soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Lumenal (Potential).
Catalytic subdomain A.
Catalytic subdomain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-acetylgalactosaminyltransferase 2. Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.4%; Score 128.5; DB 1; Length 570; 55.6%; Pred. No. 7.1e-09; tive 6; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 CGGSLEIIPCSRVGHVFRKQHPYTFPGGSGTVFARNTRRAAEVWM 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / MALHNPQ (in isoform 2).
/ FTIG-VSP 011201.
R - L (in Ref. 1).
C -> Y (in Ref. 2).
DSR -> NSK (in Ref. 2).
F -> V (in Ref. 1).
F -> V (in Ref. 1).
W, 90D5DC02C85A8EEA CRC64;
subfamily.
-!- SIMILARITY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OZ-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last amnotation update)
UDP-N-accyl-alpha-D-galactosamine:polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                     EMBL, AF348968, AAK37548.1, --
EMBL, AK046567; BAC32790.1; --
EMBL, BC007172.1, --
EMBL, BC053063, AAH53063.1; --
EMBL, BC059818, AAH59818.1; --
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518
564
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570 AA;
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tes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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226244440
24624466
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SEQUENCE
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DISULFID
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
AAH59818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Michael Manner Colling F. M. Grouse L. H., Derge J. G. M. Schler G. D. M. Strausberg R. L. Feingold E. A., Grouse L. H., Derge J. G., Schler G. G. Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G., Schler G. D., Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K., A histohul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K., A hoppins R.F., Jordan H., Moore T., Max S. J., Wang J., Hsieh F., A Diatchenko L., Marusina K., Farner A. A., Rubin G. M., Hong L., Stapleton M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E., A Brownstein M. J., Usdin T. B., Toshlyuki S., Carnino P. M., Malahy S. J., Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunarache P. H., A Richards S. Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W., A Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G. G., Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C., A Butterfield Y. S. N., Krzywinski M. I., Skalska U., Smailus D. E., Schnerch A., Schnetz J., Myers R. M., Generation and initial analysis of more han 15,000 full-length human and mouse CDNA sequences. ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12438318; DOI=10.1074/jbc.M211097200;

I wasski H., Zhang Y., Tachibana K., Gorch M., Kikuchi N., Kwon Y.-D.,

Togayachi A., Kudo T., Rubota T., Narimatsu H.;

Togayachi A., Kudo T., Rubota T., Narimatsu H.;

Togayachi A., Kudo T., Rubota T., Narimatsu H.;

Togayachi A., Kudo T., Rubota S., Gorch M., Kikuchi N., Kwon Y.-D.,

Togayachi A., Maran synthesis, In 1941 hinge region is determined by a single enzyme, UDP-N-acetyl-alpha-D-galactosaminyltransferase 2.";

To a single enzyme, UDP-N-acetyl-alpha-D-galactosamine residue to a serine or threonine residue on the protein receptor. Has a broad spectrum of substrates for peptides such as EA2, MucJa, Muclb, Probably involved in O-linked glycosylation of the immunoglobulin Al (1941) hinge region.

C. -I. CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: There are two conserved domains in the glycosyltransferase region: the N-terminal domain (domain A, also called GT1 motif), which is probably involved in manganese coordination and substrate binding and the C-terminal domain (domain B, also called Gal/GalNAc-T motif), which is probably involved in catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9295285;
Wandall H.H., Hassan H., Mirgorodskaya E., Kristensen A.K.,
Roepstorff P., Bennett E.P., Nielsen P.A., Hollingsworth M.A.,
Burchell J., Taylor-Papadimitriou J., Clausen H.,
"Substrate specificities of three members of the human UDP-N-acetyl-alpha-D-galactosamine: Polypeptide N-acetylgalactosamine: Polypeptide N-acetylgalactosaminpitransferase
[Emnly, GalNAc-TI, -TZ, and -T3.",
J. Biol. Chem. 272:23503-23514(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roctiger S., White J., Wandall H.H., Olivo J.-C., Stark A., Bennett B.P., Whitehouse C., Berger B.G., Clausen H., Nilsson T., "Localization of three human polypeptide GalNAc-transferases in HeLa cells suggests initiation of O-linked glycosylation throughout the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type II membrane protein. Golgi, resides preferentially in the trans and medial parts of the Golgi stack. secreted form also exists.
TISSUE SPECIFICITY: Widely expressed.
                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UDP + N-acetyl-D-galactosaminyl-polypeptide.
COFACTOR: Manganese and calcium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Golgi apparatus.";
J. Cell Sci. 111:45-60(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Glycosylation.
                                                           Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9394011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
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                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROWN.A.

SEQUENCE 57BJ/6; TISSUE-Brain;

MEDLINE=2238825; PubMed=1247932;

MEDLINE=238825; PubMed=12482;

MEDLINE=23825; PubMed=12482;

MEDLINE=23825;

MEDLI
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Olocypay, Olocypay,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Gastric carcinoma;
MbEDINES=96025800; PubMed=7592619;
White T., Bennett E.P., Paul E., Takio K., Sorensen T., Bonding N.,
Clausen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and cDNA cloning of a human UDP-GalNAC:polypeptide N-
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 128.5; DB 2; Length 570;
Pred. No. 7.1e-09;
6; Mismatches 11; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 CGGSLEIIPCSRVGHVFRKQHPYTFPGGSGTVFARNTRRAAEVWM 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC059818; AAH59818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                570 AA; 64514 MW; 90D5DC02C85A8EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetylgalactosaminyltransferase.";
J. Biol. Chem. 270:24156-24165(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.67
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A
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Transferase.
    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse
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RESULT 12
GLT2 HUMAN
IDT2 HUMAN
DT 01-0CTDT 01-0CTDT 01-0CTDT 01-0CTDE GAINAC
DE GAINAC

Last sequence update) Last annotation update)

Created)

PRELIMINARY;

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Năme=agCG47419; ORFNames=ENSANGG0000013497;
Anopheles gambiae Etr. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS---LARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                  preliminary data.

EMBL, AAABO108849; EAA07231.1; -.

InterPro; IPR001173; Glyco_trans_2.

InterPro; IPR000772; Ricin_B_lectin.

Pfam; PF00525; Glycos_transf2; 2.

Pfam; PF00525; Ricin_B_lectin, 4.

PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.7%;
Matches 27; Conservative
                                                                  01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                STRAIN=PEST
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SEQUENCE
                                        Q7QDR0
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AAS64620
            RESULT 13
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way wolfied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         Calcium; Direct protein sequencing; Glycosyltransferase; Golgi stack;
Lectin; Manganese; Polymorphism; Signal-anchor; Transferase;
reaction and UDP-Gal binding (By similarity).
--- DOMIN: The ricin B-type lectin domain binds to GalNAc and contributes to the glycopeptide specificity (By similarity).
--- SIMILARITY: Belongs to the glycosyltransferase family 2. GalNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypelicae Nacetylgalactosaminyltransferase 2, soluble form.

Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).

Catalytic subdomain A.
Catalytic subdomain B.
Ricin B-type lectin.
Not glycosylated (Probable).
By similarity.
By similarity.
V.-> M (in AbSND:2273970).
/FTId-WAR 019575.
T.-> G (in Ref. 1; AA sequence).
R.-> A (in Ref. 1; AA sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Removed in soluble polypeptide N-acetylgalactosaminyltransferase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%; Score 128.5; DB 1; Length 571; larity 55.6%; Pred. No. 7.1e-09; Conservative 6; Mismatches 11; Indels 3:
                                                            subfamily.
-!- SIMILARITY: Contains 1 ricin B-type lectin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide N-
                                                                                                                                                                                                                                EMBL, AL078646; CACO0585.1; -
EMBL, AL136988 -; NOT ANNOTATED CDS.
EMBL, AL117349; -; NOT ANNOTATED CDS.
EMBL, BC041120; AAH41120.1; -
FIR, 137465; 137465.
HSSP; P26514; IKNM.
Genew, HGNC:4124; GALNT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64732 MW;
                                                                                                                                                                                                                    EMBL; X85019; CAA59381.1; -.
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210
2291
2291
5222
533
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513
555
555
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533
571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
                                                                                                                                                                                                                                                                                                                                       602274;
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CONFLICT
SEQUENCE
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DISULFID
DISULFID
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TRANSMEM
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Gaps

9

Length 1003;

Score 128; DB 2; Length 10 Pred. No. 1.5e-08; 6; Mismatches 7; Indels

1003 AA; 115923 MW; 753EA50F567A4E13 CRC64;

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MEDLINE=20196006; PubMed=10731132;
MADLINE=20196006; PubMed=10731132;
MADLINE=20196006; PubMed=10731132;
MADLINE=20196006; PubMed=10731132;
MADLINE=20196006; PubMed=10731132;
MADLINE=20196006; PubMed=10731132;
MADLINE=20196006; Matches S.E., Holt R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Handerson S.N., Sutron G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X.,
MADLINE, Rogers Y.H., Blazej R.G., Change M., Pfeitfer B.D.,
MADLINE, Masun A., Handers, Prannkoch C., Baldwin D.,
Ballew R.M., Beano P.V., Berman B.P., Bhandari D., Bolshakov S.,
Barkova D., Botchan M.R., Bouck J., Broktein P., Brotter P.,
Burtis K.C., Cawley S., Daulke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Abello R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann M.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha;
Dphydroidea, Drosophila,
NCBI_TaxID=7227;
01.APR-2004 (TrEMBLrel. 27, Created)
01.APR-2004 (TrEMBLrel. 27, Last sequence update)
01.APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                          590 AA.
                                                                                                                            PRT;
                                                                                                                            PRELIMINARY;
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CG3254.
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2,

Gaps

3,

1 CGGRMEDIPCSRVGHIYRKYVPYKVP--AGVSLARNLKRVAD-WM 42

345

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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Hewland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., Morris J., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Pacleb J.M.,
Nelson D.K., Nelson K.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
She E., Siden Kiamos I., Simpson M., Skrupski M.P., Smith T.,
Shue B.C., Stapleton M., Strong R., Sun B.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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The genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacied J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
Weinska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; PubMed=12537573;
Maminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Hudang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.5%; Score 126.5; DB 2; Length 590; 55.6%; Pred. No. 1.4e-08; ative 5; Mismatches 12; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003580; AAS64620.1; -.
SEQUENCE 590 AA; 65543 MW; 4E25C39CC3A9F3D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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PubMed=12829714;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Zhang Z.;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Zhang Z.;
Ten Hagen K.G., Tran D.T., Gerken T.A., Stein D.S., Denograter of the "Punctional Characterization and Expression Analysis of Members of the "Drosophila melanogaster.",
Drosophila melanogaster.",
J. Biol. Chem. 278:35039-35048 (2003).
EMBL, AY268064, AA2657000.1, ...
Glycosyltransferase; Transferase.
SEQUENCE 615 AA; 68504 MW; BF2288312C090FEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%; Score 126.5; DB 2; Length 615; 55.6%; Pred. No. 1.4e-08; ive 5; Mismatches 12; Indels 3;
                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 CGGSLEIIPCSRVGHVFRKRHPYTFPGGSGNVFARNTRRAAEVWM 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                       Ephydroidea; Droi
NCBI_TaxID=7227;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (EC

2.4.1.41). PGANT2.

615 AA.

PRT;

PRELIMINARY;

AAQ56700 AAQ56700

RESULT 15

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AAQ56700

368 CGGSLEIIPCSRVGHVFRKRHPYTFPGGSGNVFARNTRRAAEVWM 412

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25; Conservative

Matches

Local Similarity

1 CGGRMEDIPCSRVGHIYRKYVPYKVPAGVS--LARNLKRVAD-WM 42

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NESCUENCE 2-991A-33025

Sequence 33025, Application US/09252991A

Sequence 33025, Application US/09252991A

Sequence 33025, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT:

MARC J. RUDENTION:

TITLE OF INVENTION:

TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-084-303B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 61.1
Matches 11; Conservative
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Sequence 2587, Ap
Sequence 6379, Ap
Sequence 6379, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 5230, Ap
Sequence 5230, Ap
Sequence 5230, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 27, Appl
Sequence 22, Appl
Sequence 26, Appl
                                                                                                                  November 10, 2004, 12:32:37; Search time 12.7807 Seconds (without alignments) 191.991 Million cell updates/sec
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(/cgn2_6/ptodata1//iaa/5A_COMB.pep:*

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(/cgn2_6/ptodata1//iaa/PCTUS_COMB.pep:*

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5.1.6
Compugen Ltd.
                                                                                                                                                                                                US-10-092-750-33
203
1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP
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US-09-252-991A-33025
US-09-252-991A-33025
US-09-328-352-6373
US-09-328-356-2068
US-09-328-328-2068
US-09-328-328-2068
US-09-328-328-2015
US-09-248-796A-20115
US-09-270-767-3691
US-09-396-149-14
US-09-396-149-14
US-09-396-149-12
US-09-252-991A-31215
US-09-252-991A-31215
US-09-252-991A-31215
US-09-252-991A-31215
US-09-252-991A-31215
US-09-252-991A-3133
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US-09-543-681A-7438
US-09-252-991A-23106
US-08-311-731A-106
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GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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No.
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26.6%; Score 54; DB 4; Length 106; 61.1%; Pred. No. 1.3; cive 3; Mismatches 4; Indels

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Sequence 2. Application US/09084303B

Sequence 2. Application US/09084303B

Sequence 2. Application US/09084303B

Sequence 2. Application US/09084303B

Sequence 2. Application Sequence Sequenc
                                            Sequence 9, Appli
Sequence 11, Appl
Sequence 29806, A
Sequence 2615, Ap
Sequence 50650, A
Sequence 50650, A
Sequence 50, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 15, Appl
                   Sequence
                      US-09-759-875-8

US-08-102-865-11

PCT-US92-10885-11

US-09-252-991A-29806

US-09-274-000C-5515

US-09-270-767-35435

US-09-270-767-50550

US-09-270-767-50550

US-09-270-767-50550

US-09-270-767-50550

US-09-270-767-50550

US-09-270-991A-17379

US-09-252-991A-17379

US-09-933-561-15

US-09-933-561-15

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US-09-933-561-15

US-09-933-561-15
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32986
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nes 10; Conserv
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nes 16; Conserv
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US-09-252-991A-32986
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                                                                                                                                                                                                                                                                                                     Sequence 25877, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMOMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8229
LENGTH: 263
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                                                                 DB 4; Length 416;
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24.1%; Score 49; DB 4; Length 263;
Best Local Similarity 28.6%; Pred. No. 22;
Matches 10; Conservative 11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.1%; Score 51; DB 4; Length 669; Best Local Similarity 34.5%; Pred. No. 32; Matches 10; Conservative 6; Mismatches 13; Indels
                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 SIIFLKQEEKMELLLSNSTLPGKAWLEHALPLIA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCA 35
                                                                 Score 53; DB 4; Pred. No. 9.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 ALFHVDLDPGLDHFLGDFRLAPGEADLHH 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALSWIEMDTEMEMLLARFRRTPGDLHLDH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8529, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                254 RRRAGSLPLSRRVALCAHP 272
                                                                                                                                                        19 RRTPGDLHLDHSVHLCAHP 37
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8529
                                                                 Query Match 26.1%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                            US-09-252-991A-25877
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RESULT 5

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Sequence 3731, Application US/0932832

GREATEL NROWNICH.

APPLICANT: GREAT MISSING CASA AND MINO KID SEQUENCES RELATING TO ACINSTORATER
TITLE RESERVENCE CONSTRUCT.

FILE OF INVESTIONS.

FILE OF INVESTIONS.
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANC

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20015

LENGTH: 653
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Fatent No. 6703491

GENERAL INFORMATION:

APPLICANT Homburst et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT PILION NUMBER: US/09/270,767

CURRENT PILION DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFFWARE: Patentin Ver. 2.0

SEQ ID NO 36931

LENGTH: 66
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REPERENCE: FILE REFERENCE: FILE REPERENCE: FILE RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; DB 4;
1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47.5; Di
Pred. No. 1.1e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSV 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.2%; Score 47; 37.0%; Pred. No. 8
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Application US/09248796A
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Sequence 52148, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
US-09-270-767-52148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.4%;
Best Local Similarity 38.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT Candida albicans US-09-248-796A-20015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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Matches 10; Conserv
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US-09-270-767-36931
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Patent No. 6673910

GENERAL INFORMATION:
APPLICANY: GATY L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
SEQ ID NOS: 3840
LENGTH: 288
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US-09-328-352-5330

Sequence 5230, Application US/09328352

Sequence 5230, Application US/09328352

GENERAL INFORMATION:
TITLE OF INVENTION: Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE REPRENCE: GTS-9-03P

FILLE REPRENCE: GTS-9-03P

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 353
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                                                                                                                                                                                                                                                                        Length 172;
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Pred. No. 43;
                                                                                                                                                                                                                                                                     Score 48; DB 4;
Pred. No. 19;
3; Mismatches
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      NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 MRLKRVQLTPNDMHSDKSV 287
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-5230
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                                                                                                        LENGTH: 172
TYPE: PRT
CRGANISM: mosquito baculovirus
US-09-345-236B-16
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57.1%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                87 PNDIPLDHTIRLC 99
                                                                                                                                                                                                                                                                                                                                                                                                         22 PGDLHLDHSVHLC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: M.catarrhalis
US-09-540-236-2068
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
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US-09-248-796A-20015
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US-09-540-236-2068
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Sequence 12. Application US/09396149

Sequence 12. Application US/09396149

Patent No. 6538176

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENITOR: Maize Replication Protein A and Use
FILE REFERENCE: 5718-59

CURRENT APPLICANTION NUMBER: US/09/396,149

CURRENT FILING DATE: 199-09-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12

LENGTH: 273

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
23.2%; Score 47; DB 4; Length 273;
Best Local Similarity 30.8%; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels
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23.2%; Score 47; DB 4; Length 273;
Best Local Similarity 30.8%; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels
23.2%; Score 47; DB 4; Length 66; 37.0%; Pred. No. 8.5; Live 1; Mismatches 8; Indels
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Fatent No. 6538176
GENERAL INFORMATION:
GENERAL INFORMATION:
FILLE OF INVENTION: Maize Replication Protein A and Use
FILE REPERSENCE: 5718-59
FURRENT APPLICATION NUMBER: US/09/396,149
CURRENT APPLICATION NUMBER: US/09/396,149
CURRENT APPLICATION NUMBER: US/09/396,149
SOFTWARE OF SEQ ID NOS: 22
SOFTWARE FASTSEQ FOR Windows Version 3.0
SEQ ID NO 14
LENGTH: 273
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Patent No. 6538176
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
TITLE OF INVENTION: Maize Replication Protein A and Use
FILE REFERENCE: 5718-59
CURRENT APPLICATION NUMBER: US/09/396,149
                                                                                                   19 RRTPGDLHLD-----HSVHLCAHP 37
                                                                                                                                                RHGPNSWYLDGGLRLCSHHSYHQCTHP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 DIDLHTQVLNFFNEPANLESEHGVHV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 DTDLHTQVLNFFNEPANLESEHGVHV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 DTEMEMLLARFRRTPGDLHLDHSVHL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 DIEMEMLLARFRRIPGDLHLDHSVHL 33
                          Best_Local Similarity 37.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Zea mays
US-09-396-149-12
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ORGANISM: Zea mays

US-09-396-149-14
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  Query Match
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; CURRENT FILING DATE: 1999-09-15;
; NUMBER OF SEQ ID NOS: 22;
; SOFTWARE: FastSEQ for Windows Version 3.0;
; SEQ ID NO 16;
; LENGTH: 273;
; ORGANISM: Zea mays
; ORGANISM: Zea mays
US-09-396-149-16
Query Match
Best Local Similarity 30.8%; Pred. No. 45;
Matches 8; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
Qy 8 DTEMEMLIARPRRIPGDLHIDHSVHL 33

Qy 8 DTEMEMLIARPRRIPGDLHIDHSVHL 33

Search completed: November 10, 2004, 13:44:05
Job time: 12.7807 secs
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November 10, 2004, 16:36:12 ; Search time 39.7478 Seconds (without alignments) 328.807 Million cell updates/sec
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| cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
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1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 33, Appl	Sequence 357905,	Sequence 167475,	Sequence 122236,	Sequence 167473,	Sequence 118, App	Sequence 118, App	Sequence 2, Appli	Sequence 5412, Ap	Sequence 104186,	Sequence 157136,	Sequence 350053,	Sequence 3101, Ap
ΩI	US-10-092-750-33	US-10-425-115-357905	US-10-437-963-167475	US-10-437-963-122236	US-10-437-963-167473	US-09-205-658-118	US-09-963-693-118	US-10-339-740-2	US-09-864-408A-5412	US-10-437-963-104186	US-10-424-599-157136	US-10-425-115-350053	US-10-369-493-3101
DB	14	17	16	16	16	δ	10	14	11	16	15	17	14
% Query Match Length DB I	37	141	1703	213	1136	106	106	106	130	1431	20	50	338
% Query Match	100.0	30.5	27.8	27.3	27.3	26.6	26.6	26.6	26.4	26.4	26.1	26.1	26.1
Score	203	62	56.5	55.5	55.5	54	54	54	53.5	53.5	53	53	53
Result No.	; ; ; ;	73	ო	4	Ŋ	9	7	80	מ	10	11	12	13

227 227 238 248 248	equence 162657 equence 2513, quence 46, App equence 263163 equence 14858,	7892, 339874 150072 339875 137001	8 2 2 3 3 4 7 5 6 5 6 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6	Sequence 1015, Ap Sequence 1015, Ap Sequence 1015, Ap Sequence 20731, Sequence 63033, A Sequence 39428, Sequence 39428, Sequence 37539, A Sequence 37539, A
US-09-764-847-727 4 US-10-092-154-727 5 US-10-425-114-385 7 US-10-425-115-361 4 US-10-156-761-845	US-10-437-963-1626 US-10-264-237-2513 US-09-893-737-46 US-10-425-115-2631 US-10-156-761-1485	1 US-09-86 7 US-10-42 5 US-10-42 7 US-10-42 6 US-10-43	4 US-10-043-487-28 5 US-10-424-599-23 5 US-10-424-599-23 5 US-10-425-114-66 6 US-10-437-963-12 6 US-10-156-761-71 7 US-10-156-761-71 8 US-10-156-761-71 9 US-10-156-761-71 10-424-599-24	US-10-425-299-1015 US-09-925-299-1015 US-09-925-299-1015 US-10-30-928-1015 US-10-767-701-63033 US-10-767-701-63033 US-10-725-115-18804 US-10-725-115-18804 US-10-725-115-19804 US-10-615-659-5
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ALIGNMENTS

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US-10-092-750-33

Sequence 33, Application US/10092750

Publication No. US2003002157A1

GENERAL INFORMATION:

Publication APPLICANT: Hammond, Philip W.

APPLICANT: Hammond, Philip W.

APPLICANT: Wright, Martin C.

TITLE OF INVENTION: POLYBeptides Interactive with BCL-XI

FILE REPERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT APPLICATION NUMBER: US 60/274,526

PRIOR APPLICATION
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Db 1 ALSWIEMDTEWEMILARFRRTPGDLHLDHSVHLCAHP 37
RESULT 2
US-10-425-115-357905

Sequence 357905, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:

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APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Www. Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: Bi, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS OF INVENTION NUMBER: US/10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167473
                                                                                                                                                                                            APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122236
LENGTH: 213
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US-10-437-963-122236
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US-10-437-963-167473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.3%; Score 55.5; DB 16; Best Local Similarity 43.8%; Pred. No. 10; Matches 14; Conservative 4; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 IEMD-QVAMAIDR----PIDRHLHHQLRTCAH 145
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Publication No. US20040123343A1
GENERAL INFORMATION:
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Patent No. US20010029617A1
               Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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APPLICANT: Ogg, Scott
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                                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Go, Yongwei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Brabazuk, Brad
APPLICANT: Bring Sark, Brad
APPLICANT: Bring Sark, Brad
APPLICANT: APPLICANT: A.
APPLICANT: APPLICANT: A.
APP
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant David K.
APPLICANT: David K.
APPLICANT: David X.
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 357905
LENGTH: 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%; Score 62; DB 17; Length 141; 37.8%; Pred. No. 0.7; tive 5; Mismatches 18; Indels
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US-10-437-963-167475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALSWIEMDTEMEMLLARFRRTPGDIHLDHSVHLCAHP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , CTHER INFORMATION: Clone ID: MRT4577_8957C.1.pep
US-10-425-115-357905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEX: unsure
LOCATION: (1)..(141)
OTHER INFORMATION: unsure at all Xaa locations
FARTURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-437-963-122236
; Sequence 122236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 37.8<sup>†</sup>
Matches 14<sup>‡</sup> Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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APPLICANT: La Rosa, Thomas J.

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US-10-339-740-2
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Publication No. US20030181364A1

GRARRAL INFORMATION:

APPLICANT: Ruvkun, Gary

CURRENT PILING: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS

FILE REFERENCE: 00786/351004

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US/09/205,658

PRIOR PILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: US/88,534

PRIOR APPLICATION NUMBER: US/88,534

PRIOR APPLICATION NUMBER: US/88,10080

PRIOR PILING DATE: 1997-07-07

PRIOR APPLICATION NUMBER: US/88/10080

PRIOR PILING DATE: 1999-05-15

NUMBER OF SEQ ID NOS: 328

SOFTWARE: FBSESEQ for Windows Version 4.0

COCANTENT: DO 108

LENGTH: DO
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TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS FILE REFERENCE: 0786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/88,534
EARLIER FILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US/08/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTMARE: FEASUSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Caenorhabditis elegans
US-09-205-658-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
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APPLICANT: Reddy, Bindu
APPLICANT: Platt, Darren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 iEMETELENQLSRARRVP
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Best Local Similarity
Matches 11, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-963-693-118
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US-09-963-693-118
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 118
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US-10-339-740-2
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TITLE OF INVENTION: UNCERTED ALDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND US TITLE OF INVENTION: THEREOF TITLE OF TITLE APPLICATION NUMBER: US/09/084,303A PRIOR APPLICATION NUMBER: US/09/084,303A PRIOR APPLICATION NUMBER: US/09/084,303A PRIOR FILING DATE: 1998-05-26 SOFTWARE: PARCH FILING DATE: 1998-05-26 SOFTWARE: PARCH TING DATE: 1998-05-26 TITLE DATE: 1998-05-26 TITLE DATE: 1998-05-26 SOFTWARE: PARCH TING DATE: 1998-05-26 SOFTWARE: 1998-05-26 SOF
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APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NO. US20040009474Alel Human Polynuclectides and Polypeptides Encoc FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5412
LENGTH: 130
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Sequence 104186, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbaauk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement.
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26.6%; Score 54; DB 14; Length 106;
Best Local Similarity 61.1%; Pred. No. 7.6;
Matches 11; Conservative 3; Mismatches 4; Indels
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; Sequence 5412, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
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Ferguson, Kimberly
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; ORGANISM: Homo sapiens
US-09-864-408A-5412
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US-10-437-963-104186
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Ainkle, Gregory J.
APPLICANT: Slacer, Seeven C.
APPLICANT: Slacer, Seeven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TILLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3101
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.1%; Score 53; DB 14; Length 338;
Best Local Similarity 25.0%; Pred. No. 39;
Matches 13; Conservative 6; Mismatches 11; Indels 22; Gaps
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Factor No. US2000132767A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOP;
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT PILING DATE: 2001-01-17
FILE OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
IENGTH: 51
IENGTH: 51
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     DB 17; Length 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (1). (338)
COTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3101
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                                                  3; Mismatches
  Query Match
26.1%; Score 53; D
Best Local Similarity 52.4%; Pred. No. 5.
Matches 11; Conservative 3; Mismatche
                                                                                                                                                                                                                                                           Sequence 3101, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                             21 TPGDLHLDHSVH----LCAHP 37
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ORGANISM: Neurospora crassa
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US-09-764-847-727
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US-10-369-493-3101
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US-09-764-847-727
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US-10-424-59-157136

Sequence 157136, Application US/10424599

Publication No. US20040031072A1

GENERAL INPORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Thou Yihua

APPLICANT: Cov Yongwi

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement

FILE REPERRNCE: 38-21(53.22) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 157136

LENGTH: 50
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 350053
LENGTH: 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101544C.1.pep
US-10-437-963-104186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; CTHER INFORMATION: Clone ID: PAT_MRT3847_112915C.1.pep
US-10-424-599-157136
                                                                                                                                                                                                             Query Match 26.4%; Score 53.5; DB 16; Best Local Similarity 45.2%; Pred. No. 1.7e+02; Matches 14; Conservative 3; Mismatches 9;
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JS-10-425-115-350053
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104186
LENGTH: 1431
                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
FEATURE:
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RESULT 15

US-10-092-154-727

i Sequence 727, Application US/10092154

i Publication No. US20030054375A1

i GENERAL INFORMATION:

i TITLE OF INVENTION:

i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

i CURRENT APPLICATION NUMBER: US/10/092,154

CURRENT FILING DATE: 2002-03-07

i NUMBER OF SEQ ID NOS: 2003

i Prior Application removed - See File Wrapper or Palm

SOFTWARE: PATH

i CURRENT ST.

i DENGTH: 51

i TYPE: PRT

i ORGANISM: Homo sapiens

US-10-092-154-727

Query Match

Best Local Similarity 27.3%; Pred. No. 6.5;

Matches 9; Conservative 5; Mismatches 19; Indels

QY 4 WIEMDTEMEMILARFRETEGDLHLDHSVHLCAH 36

| HIRDEMORTALVILPEXCLERELPRATHTHTHTTCSH 36

| HIRDEMORTALVILPEXCLERELPRATHTHTHTTCSH 36

| HIRDEMORTALVILPEXCLERELPRATHTHTHTTCSH 36
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Search completed: November 11, 2004, 01:28:15 Job time : 40.7978 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32 ; Search time 8.24352 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-33 203 1 ALSWIEMDTEMEMLLARPRRTPGDLHLDHSVHLCAHP 37

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ф			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
,	09	9	. 4	~	G83976	cytochrome caa3 ox
7	55.5	27.3	~	~	T22615	cal pro
٣	55	27.1	199	N	S16063	acp-22 protein - y
4	55	27.1	σ	7	S32224	acp-22 protein - y
S	54	9	0	7	T27989	hypothetical prote
9	52.5	5	ထ	7	T35469	probable ATP /GTP-
7	52	'n,	വ	7	AF1372	proteins involved
80	52	δ.	S	N	AD1742	protein involved i
σ	52	ď.	4	~	C45335	cytochrome-c oxida
10	52	5	σ	7	E36792	hypothetical prote
11	51.5	δ.	4	7	T51959	hypothetical prote
12	Η.	ď.	Н	7	S26845	dīmp kinase (ĒC 2.
13	51	S.	4	7	E69392	glucose-1-phosphat
14	51	ъ.	9	Н	C55973	transcription fact
15	51	S	4	~	A71347	hypothetical prote
16	51	ď.	σ	7	D83472	probable glycosyl
17	51	5.	-	7	S60676	cellobiose oxidase
18	20	4	4	ď	T29819	hypothetical prote
19	20	4	Ø	N	A28569	alpha-methyldopa-h
20	20	4.	н	7	F85095	hypothetical prote
21	50	4.	0	7	T49577	hypothetical prote
22	ď.	4.	4	7	C82508	hypothetical prote
23	49.5	4	44	Н	JVBPAL	DNA-packaging prot
24	6.	24.4	4	N	H85689	terminase large su
25	σ,	24.4	4	N	F90832	terminase large su
56	σ,	24.4	ゼ	N	C90901	probable terminase
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28	49	4	LO.	N	C83814	ciporte
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hypothetical prote	conserved hypothet	hypothetical prote	DnaJ-like protein	hypothetical prote	ATP-dependent heli	probable membrane	conserved hypothet	malonyl-CoA transa	3-deoxy-D-manno-oc	NADH2 dehydrogenas	hypothetical prote	interferon-induced	probable pdc prote	probable transcrip	DNA-directed RNA p
A97640	AB2863	T34406	T09338	867621	H83873	867053	G69158	T44805	E83023	T11515	T12515	A25407	E70814	C87128	865068
~	~	~	7	N	N	N	~	N	~	7	~	0	~	~	7
251	251	339	423	545	643	116	277	400	425	459	352	478	260	1106	1191
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49	49	49	49	49	49	49	48.5	48.5	48.5	48.5	48	48	48	48	48
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ALIGNMENTS

To the casa oxidase (subunit II) ctac (imported) - Bacillus halodurans (sees Bacillus halodurans) 10.1-Bec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 10.10-Bec-2000 #sequence_revision 0.5: Sasaki, R.; Masui, N.; Fuj 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G83976 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G83976 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G83976 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G83976 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G83976 10.10-Bec-2000 #sequence of the alkaliphilic bacterium Bacillus haloession: G999 #sequence for Bec-2000 #sequenc	DECITE 1	
C.Species Bachline halodurans C.Species Bachline halodurans C.Species Bachline halodurans C.Species Bachline halodurans C.Accession: 63396 R.Takani, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; R.Takani, H.; Makasone, R.; 4317-4311, 2000 A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A.Reference number: A33550; MUID:20512582; FWID:11058132 A.Accession: 633976 A.Accession: 632976 A.Accession: 722615 A.Accession: 72261	caa3 oxidase (subunit II) ctaC [imported] -	alodurans (strain C-125)
Nuclear Acids Res. 28, 417-431, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nuclear Acids Res. 28, 417-431, 2000. A. Muclear Acids Res. 28, 417-431, 2000. A. Matter Complete grames sequence of the alkaliphilic bacterium Bacillus halodurans A. Matter complete grames sequence of the alkaliphilic bacterium Bacillus halodurans A. Macession. G83376 A. Macesion. G83376 A. Macesion. G83376 A. Macesion. Tasake S. Tron, membars. 1734 6.300. A. Macesion of thromoprotein, copper 2 (Cys. GB., Cys. Has) Haratus predicted C. Superfamily: optochrome-coxidase chain II, cytochrome c containing; cytochrome c C. Superfamily: optochrome-coxidase chain II, cytochrome c containing cytochrome c C. Superfamily: optochrome-coxidase chain II, cytochrome c containing cytochrome-coxidase chain II, cytochrome c containing cytochrome c C. Superfamily: optochrome-coxidase chain II, cytochrome c C. Superfamily: optochrome-coxidase correlation of Cytochrome c C. Superfamily: optochrome-coxidase conservative conservative 2; Mismatches 6; Indels 0; Gaps 0; Matches II; Conservative 2; Mismatches 6; Indels 0; Gaps 0; IIIARRRKPCODELERQUY 85 RESULT 2 RESULT 3 RESULT 4 RESULT 5 RESULT 5 RESULT 5 RESULT 5 RESULT 5 RESULT 5 RESULT 6 RESULT 6 RESULT 7 R	C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-J	9-Jul-2004
A; Filtle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83550; MUID:20512582; FMID:11058132 A; Accession: G83976 A; Status: preliminary A; Motecule type: DAA A; Status: preliminary A; Motecule type: DAA A; Status: preliminary A; Motecule type: DAA A; Cross-references: UNTROT:QSKNO; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:B A; Moterimental source: strain C-125 C; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c C; Superfamily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c C; Superfamily: cytochrome-c oxidase chain II, cytochrome c C; Superfamily: cytochrome-c C; S	C.ACCESSION: 0537/9 R.Takami, H.: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui Nucleic Acids Res. 28, 4317-4331, 2000	sui, N.; Fuji, F.; Hiran
A;Status; preliminary A;Status; preliminary A;Status; preliminary A;Readdes: 1.348 e200. C;Generics: A;Gene: ctac C;Superiamily; cytcohrome-c oxidase chain II, cytcohrome c containing; cytcohrome c c;Reynocds: cincin predicted containing site: copper 2 (Cyg. dlu, Cyg. Has) #status predicted C;Superiamily: cytcohrome-coxidase chain II, cytcohrome c circohrome circo	A,Title: Complete genome sequence of the alkaliphilic bacterium Baci A,Reference number: A83650; MUID:20512582; PMID:11058132 1.B.Cession: G81374	acillus halodurans and ç
A, Reselvences: 1-348 cSTO> A, Reselvences: UNIPOCT: O9KSNO; GB: AP001516; GB: BA000004; NID: g10175192; PIDN: B. A; Cross-references: UNIPOCT: O9KSNO; GB: AP001516; GB: BA000004; NID: g10175192; PIDN: B. C; Genetics: ctac C; Genetics: ctac C; Genetics: ctac C; Superafamily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c C; Superafamily: Cytochrome c C; Seywords: chromoprotein; copper; electron transfer; heme; iron; membrane-associat F; 210. 210, 211, 211, 217) Hinding site: copper; electron transfer; heme; iron (His) (axial ligand) #status predicted F; 211/Binding site: heme (Cys) (covalent) #status predicted F; 271/Binding site: heme (Cys) (covalent) #status predicted Cyse: 12 Conservative 2; Mismatches 6; Indels 0; Gaps 0; Db 66 IIIARPREKEGDBELPKQVH 85 ERSULT 2 Cype: 13 MILARPREKEGDBELPKQVH 85 C; Gate: 13-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T22615; T24303 C; Accession: T22615; T24303 C; Accession: T22615; T24303 C; Accession: T22615; T24303 A; Reference number: 219589 A, Accession: T22615 A; Reference number: 219589 A, Refe	A;Status: preliminary A;Molecule type: DNA	
C.Genetics: A.Genetics: A.Genetics: C.Genetics: C.Genetics: C.Genetics: C.Genetics: C.Genetics: C.Superfamily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c C; Superfamily: cytochrome-c coper c C; Superfamily: cytochrome-sescotat C; Superfamily: cytochrome c C; Superfamily: cytochrome c C; Superfamily: cytochrome stee: or		:g10175192; PIDN:BAB063
Cisuperfemily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c Cisuperfemily: cytochrome-c oxidase chain II, cytochrome c containing; cytochrome c Cisuperfemily: 217-20,211,213,217-20,21,217-20,21,217-20,21,217-20,21,217-20,21,217-20,	C;Genetics:	
Cixeywords: chromoprotein; copper; electron transfer; heme; iron; membrane-associat Cixeywords: chromoprotein; copper; electron transfer; heme; iron; membrane-associat F;209,211,213,212/Binding site: magnesium (Glu) (shared with chain I) #status predicted F;211/Binding site: magnesium (Glu) (shared with chain I) #status predicted F;271/Binding site: heme (Cys) (covalent) #status predicted Guery Match Site: heme iron (His) (axial ligand) #status predicted Guery Match Similarity 60.0%; pred; No. 1; Bast Local Protein TOLE8.5 - Caenorhabditis elegans C;Species: Gaenorhabditis	c;Superfamily: cytochrome-c oxidase chain II, cytochrome c containin	ning; cytochrome of home
P;267,270/Binding site: heme (Cys) (covalent) Hatatus predicted Query Match Query Match Query Match Query Match Query Match 29.6%; Score 60; DB 2; Length 348; Best Local Similarity 60.0%; Pred. No. 1; Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0; 3 MLARFRETPCDLHLDHSVH 32 13 MLARFRETPCDLHLDHSVH 35 C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 10-Oc-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 10-Oc-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 10-Oc-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 10-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 10-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 10-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 11-Oct-1999 #sequence_revision 15-Oct-1999 A; McGassion: 722615 A; McGassion: 722615 A; McGassion: 722615 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Cross-references: UNIPROT; Q20749; EMBL: Z48583; PIDN: CAA88473.1; GSPDB: GN00020; CB; McManray, A. Submitted to the EMBL Data Library, March 1995 R; McManray, A. Submitted to the EMBL Data Library, March 1995	C;Keywords: chromoprotein; copper; electron transfer; heme; iron; me F;809,211,217,215,217,81ding site: copper 2 (79, Glu, Cys, His) #statu e.7.17,71,713,712,717, minimum site: copper 2 (79, Glu, Cys, His) #statu	membrane-associated con atus predicted
Length 348; 6; Indels 0; Gaps 0; ns #text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;	F/71.75.10/Binding site: magurerum (sign) (signam with canal 1.7 #Stocked F/267,270/Binding site: heme (Cyg) (covalent) #status predicted F/271/Binding site: heme iron (His) (axial ligand) #status predicted	predicted
ns #text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;	29.6%; Score 60; DB 2; Length 348; 60.0%; Pred. No. 1; ative 2; Mismatches 6; Indels	Gaps
ns #text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;	13 MLLARFRRTPGDLHLDHSVH	
ns #text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;	::	
ns #text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;		
#text_change 09-Jul-2004 DN:CAA88473.1; GSPDB:GN00020;	hypothetical protein TOIE8.5 - Caenorhabditis elegans	
#.ext_change 09-041-2004	410	
/DDBJ 3; PIDN:CAA88473.1; GSPDB:GN00020;	#rexr_cnange	
/DDBJ 3, PIDN:CAA88473.1, GSPDB:GN00020,	Library, March	
/DDBJ 3, PIDN:CAA88473.1, GSPDB:GN00020,	A,Rererence number: 219589 A,Accession: T22615	
3; PIDN:CAA88473.1; GSPDB:GN00020;		
KimcMurray, A. submitted to the EMBL Data Library, March 1995	A;Residues: 1-1270 <wil> A;Cross-references: UNIPROT:Q20749; EMBL:Z48583; PIDN:CAA88473.1; GS A;Experimental source: clone F54B3</wil>	GSPDB:GN00020; CESP:T01
	Kinchurray, A. Submitted to the EMBL Data Library, March 1995 A:Reference number: 719871	

- Caenorhabditis elegans

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proteins involved in resistance to cholate and to NA(+) and in pH homeostasis homolog lmc proteins: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AFI372
C;Accession: 
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rossidues: 1-886 cMUR>
A,Cross-references: UNIPROT:086768; EMBL:AL031035; PIDN:CAA19923.1; GSPDB:GN00070; SCOEDE
A,Experimental source: strain A3(2)
A,Experimental source: strain A3(2)
A,Gene: SCOEDB:SC6A9.38
                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-166 <KIR>
A;Residues: 1-166 <KIR>
A;Cosa-references: UNIPROT:Q09626; EMBL:U23451; PIDN:AAC46744.1; CESP:ZK75.1
A;Experimental source: strain Bristol N2
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27989
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35469
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A; Reference number: 221578
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A,Introns: 79/1
C,Superfamily: Caenorhabditis elegans hypothetical protein ZK84.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.6%; Score 54; DB 2; Length 106; Best Local Similarity 61.1%; Pred. No. 2; Matches 11; Conservative 3; Mismatches 4; Indels
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                                                                                                                                                           Rikirsten, J. submitted to the EMBL Data Library, July 1995
A; Description: The sequence of C. elegans cosmid ZK75.
A; Reference number: Z20451
A; Reference number: Z20451
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Pred. No. 34;
2; Mismatches 10;
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36 IEMETELENQLSRARRVP 53
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ilarity 45.2%;
Conservative
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Best Local Similarity
Matches 14; Conserv
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A,Molecule type: DNA
A,Residues: 1-159 <GLA>
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A;Map position: 2
A;Introns: 15/1; 35/3; 73/3; 99/2; 237/1; 277/3; 332/3; 397/2; 534/3; 703/3; 1006/1; 119
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                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-170 (*M12>
A;Cesidues: 1-170 (*M12>
A;Cross-references: EMBL:Z48809; PIDN:CAA88749.1; GSPDB:GN00020; CESP:T01E8.5
A;Experimental source: clone T01E8
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C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acp-22 protein - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Modecule type: DNA
A;Rosidues: 1-199 <BOU>
A;Cross-references: UNIPROT:P26968; EMBL:X72783; NID:g288439; PID:g288440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S16063
R; Bouhin, H.; Charles, J.P.; Quennedey, B.; Delachambre, J.
Subnitted to the EMBL Data Library, July 1991
A; Description: Molecular cloning of a glycine-rich cuticular protein.
A; Reference number: S16063
A; Accession: S16063
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27.1%; Score 55; DB 2; Length 199;
Best Local Similarity 52.9%; Pred. No. 2.9;
Matches 9; Conservative 4; Mismatches 4; Indels
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R;Bouhin, H: Braquart, C.; Charles, J.P.; Delachambere, J. Bubmitted to the EMBL Data Library, March 1993
A;Reference number: S32224
A;Accession: S32224
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Pred. No. 2.9;
4; Mismatches
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626 ISWIEVEREMMNIDARVKRTKLKDCELYEDH 656
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TPVDVHHEEAIHLKAHP 134
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118 TPVDVHHEEAIHLKAHP 134
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity
Matches 13; Conserv
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A,Molecule type: mRNA
A,Residues: 1-199 <BOU>
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                    A; Accession: T24303
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Gaps

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Gaps

Genetics:

RESULT 5 T27989

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C;Species: Picea mariana
C;Species: Picea mariana
C;Accession: T51959
R;Perry, D.J; Bousquet, J.
Genetics 149, 1089-1098, 1998
A;Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, characteriza
A;Reference number: Z25268; MUID:9823; PMID:9611216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-599 <DAV>
A;Cross-references: UNIPROT:Q00157; GB:M75136; NID:g331209; PIDN:AAA88161.1; PID:g331268
R;Davison, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: E36792
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ORFS8 - ictalurid herpesvirus 1 (strain auburn 1)
C;Species: ictalurid herpesvirus 1
                                                            ..
0
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A,Cross-references: UNIPROT:065048, EMBL:AF051205; PIDN:AAC32110.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Note: neither protein nor nucleic acid sequence is given C,Genetics:
A,Gene: 58
C,Superfamily: ictalurid herpesvirus 1 hypothetical protein ORF58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51.5; DB 2; Length 141; Pred. No. 6.3; 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R,Davison, A.J.
submitted to GenBank, January 1992
A,Description: Channel catfish virus: a new type of herpesvirus.
A,Reference number: A36804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 599,
                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Davison, A.J.
Virology 186, 9-14, 1992
Afitle: Channel caffish virus: a new type of herpesvirus. A;Reference number: A39447; MUID:92087490; PMID:1727613
A;Contents: annotation
                                                            . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                      45.0%; Pred. No. 14; tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein [imported] - Picea mariana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 WIEMDTEMEMLLARFRRIPGDLHLDHSV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                            13 MLLARFRRIPGDLHLDHSVH 32
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dTMP kinase (EC 2.7.4.9) - human
                      Best Local Similarity 45.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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DP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    profess involved in resistance to cholate and to NA(+) and in pH homeostasis homolog ling cipecies: Listeria innocua
C;Species: 27-NOv-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1742
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Jonnes, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-159 cGIA>
A;Residues: 1-159 cGIA>
A;Residues: 1-159 cGIA>
A;Residues: L-159 cGIA>
A;Residues: L-159 cGIA>
A;Residues: L-159 cGIA>
A;Residues: L-150 cGI
A;Cross-references: UNIPROT:Q8Y4Q2; GB:NC_003210; PIDN:CAD00460.1; PID:g16411870; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2382
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome-c oxidase (EC 1.9.3.1) chain II - Bacillus firmus

C;Species: Bacillus firmus

C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C;Accession: C45335; 139821

R;Quirk, P.G.; Hicks, D.B.; Krulwich, T.A.

J. Biol. Chem. 268, 679-685, 1993

A;Title: Cloning of the cta operon from alkaliphilic Bacillus firmus OF4 and characteriz

A;Reference number: A45335; MUID:93107080; PMID:7678007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Cytochrome-c oxidase chain II, cytochrome c containing, cytochrome-c oxid C;Reywords: copper; electron transfer; heme; membrane-associated complex; oxidoreductase C;31-228/Domain: cytochrome-c oxidase chain II homology <CO2>
F;17-5,210,214,221,Binding site: copper I (His, Cys, Cys, Mis) #status predicted F;210,212,214,218/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted F;212/Binding site: magnesium (Glu) (shared with chain I) #status predicted
                                                                                                                                                                                                                                                                                                      ı;
                                                                                                                                                                                                                                                                                                      Gaps
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A;Experimental source: strain OF4
                                                                                                                                                                                                                                                                                                      10;
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Pred. No. 6.1,
5, Mismatches 11, Indels
                                                                                                                                                                                                                       Score 52; DB 2; Length 159;
Pred. No. 6.1;
5; Mismatches 11; Indels
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C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1401
                                                                                                                                                                                                                                                                                                                                                                                                                   5 IEMDTEMEMLLARFRRIPGDLHLD-----HSVHL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IEMDTEMEMLLARFRRTPGDLHLD------HSVHL 33
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                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3%;
Matches 13; Conservative
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Local Similarity 33.3%;
hes 13; Conservative
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à g

ternate names: deoxythymidylate kinase

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hypothetical protein TP0260 - syphilis spirochete
c; pagecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
c; pagecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
c; pagecies: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Accession: A71347
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDorthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Ttle: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                AjGene: is1-3
C;Superfamily: transcription factor is1-1; homeobox homology; LIM metal-binding repeat he C;Superfamily: transcription splicing; DNA binding; duplication; homeobox; nucleus; transcript F;27-80,Domain: LIM metal-binding repeat homology <LIML>
F;89-142/Domain: LIM metal-binding repeat homology <LIML>
F;192-248/Domain: homeobox homology <HOX>
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AjExperimental source: strain Nichols
R;Gong, Z.; Hew, C.L.
Biochim. Blogbhys. Acta 1260, 349-354, 1995
A;Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchu
A;Reference number: S52089; MUID:95178560; PMID:7873614
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C,Superfamily: syphilis spirochete hypothetical protein TP0260
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Local Similarity 40.0%; Pred. No. 26;
les 12; Conservative 5; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 MEMLLARFRRTPGDLHLDHSVHLCAHP 37
                                                                                                                                                                                                                                                                 <G02>
                                                                                                                                                                          A,Status: preliminary
A,Molecule type: mRNA
A,Sesidues: 1-82,'IWNKWCKMQPGIQQO'
A,Cross-references: EMBL.X64883
A,Note: alternative splice form
                                                                                                                                                      A; Accession: S52090
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                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
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Matches
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Matches
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C55973

transcription factor isl-3 - chinook salmon
NyAlternate names: insulin enhancer-binding protein isl-3; islet-3 protein
NyAlternate names: insulin enhancer-binding protein isl-3; islet-3 protein
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschawytscha (chinook salmon)
C;Species: Oncorhynchus tschamper.averision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: C55973; S52090
R;Gong, Z.; Hui, C.; Hew, C.L.
A;Title: Presence of isl-1-related LIM domain homeobox genes in teleost and their simila
A;Reference number: A55973; MUID:95155429; PMID:7852419
A;Accession: C55973
A;Accession: C55973
A;Accession: C55973
A;Accession: C55973
A;Accession: C55973
A;Cross-references: UNIPROT:P53409; GB:X64883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucose-1-phosphate cytidylyltransferase (rfbF) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: 659392 C;Accession: 659392 C;Accession: 659392 C;Accession: 659392 C; Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 344-370, 1997 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C. A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-241 <KLE>
A;Cross-references: UNIPROT:029123; GB:AE001025; GB:AE000782; NID:g2689348; PIDN:AAE901d
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P23919; EMBL:X54729; NID:g37205; PIDN:CAA38528.1; PID:g37206
                                                                                                                      C)Accession: S26845
R;Su, J.Y.; Sclafani, R.A.
Nucleic Acids Res. 19, 823-827, 1991
A;Telle: Molecular cloning and expression of the human deoxythymidylate kinase gene in )
A;Reference number: S26845; MUID:91204436; PMID:2017365
A;Accession: S26845
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-211 < SUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                   N;Alternate names: deoxythymidylate kinase
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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25.4%; Score 51.5; DB 2; Length 211; llarity 40.6%; Pred. No. 9.7; Conservative 6; Mismatches 12; Indels

Local Similarity nes 13; Conserv

ð g

Query Match Best Loca Matches

2 LSWIEMDTEMEMLLARFRRTPGDLHLDHSVHL 33

A;Map position: 2pter-2qter C;Superfamily: dTMP kinase C;Keywords: nucleotide binding; P-loop; phosphotransferase F;13-20/Region: nucleotide-binding motif A (P-loop)

A; Cross-references: GDB:127511; OMIM:188345

A; Gene: GDB: DTYMK

Search completed: November 10, 2004, 13:40:41 Job time: 9.24352 secs

Ouery Match 25.1%; Score 51; DB 2; Length 241; Best Local Similarity 42.9%; Pred. No. 13; Matches 9; Conservative 5; Mismatches 7; Indels

1-241 <KLE>

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 10, 2004, 12:27:34 ; Search time 45:1796 Seconds (without alignments) 471.205 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-092-750-33 203 1 ALSWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCAHP 37 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

cripti	:	pla.	bac	oryza sat	178 oryza	3 orvza sa	7 vibrio v	vibrio	_	_		caenor	_	rwinia	ispo		aenoz	O7px17 anopheles q	attus nor	rattu	Cae83920 rattus no	radyrhi	Q6mgs6 bdellovibri	Cae78371 bdellovib	Q6mqj4 bdellovibri	5	r	826	. 9 az	95 Jentospir	2 leptospir
	Q7RQ36	QBILG1	ON6X6O	Q7FAB9	CAE03978	Q7XEA3	Q7MCN7	Q8D5N2	Q8DHF7	68H16Ö	QBRYX8	020749	AC22 TENMO	QBKUM3	ISDF ZYMMO	Q9XTA0	ILB1 CAEEL	Q7PX17	099JC6	AAH62007	CAE83920	Q89EX1	QEMQS6	CAE78371	Q6MQJ4	CAE78453	Q6N5Z5	CAE28265	691760	72M9	OSEYT2
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081LG1 PRELIMINARY; PRT; 2657 AA. 081LG1; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

RESULT 2
Q81LG1
ID Q81LC
AC Q81LC
DT 01-M3

351 NWYSIENEEEVLRKTFRQ-PDDLHCSHHEELCS 382

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Aas71837 leptospir O86768 streptomyce	0928q1 listeria in 08v4q2 listeria mo	Q71x44 listeria mo Aat05121 listeria	004441 bacillus ps	ictalurid		O65048 picea maria		Q82pj0 streptomyce		Q6cam9 yarrowia li
AAS71837 086768	Q928Q1 O8Y4O2	Q71X44 AAT05121	COX2 BACPF	VG58_ICHV1	Q8SA <u>6</u> 9	065048	KTHY HUMAN	Q82PJ0	Q7WR40	Q6CAM9
		159 2		1 669	•	•	112 1	•	•	40 2
	25.6	6.6	25.6	25.6	2 25.6		25.4	.5 25.4	25.4	
33	3.4 3.5	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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InterPro; IPR002327; Cyt_CIAB.
InterPro; IPR002429; Cyt_c_ox_2
                                                                                                                                                                                                                           est_Local Similarity 60.0
atches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSJNBa0033H08.2 protein.
Name=OSJNBa0033H08.2;
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Matches
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Q7FAB9
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"Complete genome sequence of the alkaliphilic bacterium Bacillus
"Complete genome sequence comparison with Bacillus subtilis.";
"Nucleic Acids Res. 28:4317-4331(2000).

"Nucleic Acids Res. 28:4317-4331(2000).

"EMBL, AP001516; BAB06334.1; -.

"A GO; GO:000520; Cimembrane; IEA.

"A GO; GO:000520; Cimembrane; IEA.

"A GO; GO:000510; P:coptochrome-c oxidase activity; IEA.

"A GO; GO:000510; CytC. Leme_BS.

"A InterPro; IPR003068; CytC. Leme_BS.

"A InterPro; IPR003088; CYt. CI."
                                                                                                             MEDLINE=22555705; PubMed=12368864; Main R.W., Hyman R.W., Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K.E., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Perterson J., Angluoli S., Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mingall C., Varucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20515582; PubMed-11058132; Medline-20515582; Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                    32.8%; Score 66.5; DB 2; Length 2657; 39.4%; Pred. No. 5.5;
                   OKFNames=PP14 0282;
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                             Nature 419:498-511(2002).

EMBL, AR014820, ARN36895.1; -. EMBL, AR014820; ARN36895.1; -. Interpro. 100:003393; F:acid phosphatase activity; IEA.

Interpro. IPR000560; HisAc_phsphtse.

PROSTIS, PS00616; HIS_ACID_PHOSPHAT_1; 1.

Hyporhetical protein. 306805 MW; 4AA679A6D91877C2 CRC64; SEQUENCE 2657 AA; 306805 MW; 4AA679A6D91877C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome caa3 oxidase (Subunit II)
      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 NWYNIENBEEVLRKTFRQ-PDDLHCSHHEELCS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SWIEMDTEMEMLLARFRRTPGDLHLDHSVHLCA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 39.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                     falciparum.
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Q9K9N0
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prem; PF00116; COX2, 1.
Pfam; PF02790; COX2_TM; 1.
Pfam; PF02790; COX2_TM; 1.
Pfam; PF0014; Cytochrom C; 1.
Probom; PF000131; Copper_CuA; 1.
Probom; PF000375; Cyt_CTAB; 1.
PROSITE; PF00199; CYTOCHROME_C; UNKNOWN_1.
Electron transport; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ebrhartoideae; Oryzeae; Oryza.
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Lacture and analysis of rice chromosome 4.";

Lacture 420:316-320(2002).

R Nature 420:316-320(2002).

R EMBL; AL662942; CAE03783; -.

R InterPro; IPR0018975; Viral cap_coat.

R InterPro; IPR0018975; Viral cap_coat.

R Pfam; PF00065; rve.

R Pfam; PF000665; rve.

R Pfam; PR00099; Zf-CCHC; 1.

R PRINTS; PR0099; Zf-CCHC; 1.

R PRANTS; PS0099; Zf-CCHC; 1.

R PROSITE; PS50158; Zf-CCHC; 1.

R PROSITE; PS50158; Zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                       Length 348;
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                                                                                                                                                                                                                                                                                            SEQUENCE 348 AA; 38585 MW; EA287CD1AC9AE323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1479 AA.
                                                                                                                                                                                                                                                                                                                                                       29.6%; Score 60; DB 2 60.0%; Pred. No. 4.7; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 MLLARFRRTPGDLHLDHSVH 32
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Created)
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                                                                                                                                                                                             1708 AA; 188208 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13:2577-2587(2003).
  Pfam; PF00651; BTB; 2.
Pfam; PF00655; rve; 1.
Pfam; PF00099; zf-CCHC;
SMART; SM00225; BTB; 1.
SMART; SM00343; znF-C2HC; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8D5N2 PRELIMINARY;
Q8D5N2;
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                              Best Local Similarity 46.9
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=VVA1349;
                                                                                                                                                                       Polyprotein.
SEQUENCE 1
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Genome Res.
                                                                                                                                                                                                                                          Query Match
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Q8D5N2
ID Q8D51
AC Q8D51
DT 01-M2
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                                                                                                                                                                                                                                                                                                                                                                                              Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Liu X., Zhang L., Lu Y., Mu W., Lu Y., Zhang L., Lu Y., Mu W., Sun T., Lei H., Li T., Hu H., Guan D., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Uin Z., Wang R., Zhou B., Chen Z., Chen L., Jia J., Wang R., Yin H., Chen S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang R., Yin H., Wang L., Ding C., Sheng H., Gu G., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Han B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cuitivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnolliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzea, Oryza, Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017096, AAPS3887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATÚTE 420:316-320(2002).
EMBL; ALG62942; CAE03978.3; -.
SEQUENCE 1479 AA; 162541 MW; 8A8E584CA2A33DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 EMEMLLARFRRIPG-----DIHLDHSVHLCAH 36
                           1479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.8%; Score 56.5; 1
46.9%; Pred. No. 80;
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                           PRT;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
MEDLINE=22337377; PubMed=12447439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative gag-pol polyprotein.
ORFNames=OSJNBa0073D04.30;
                      CAE03978 PRELIMINARY;
CAE03978;
02-MAR-2004 (TEMBLEEL 27,
02-MAR-2004 (TEMBLEEL 27,
02-MAR-2004 (TEMBLEEL 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.9
Matches 15; Conservative
                                                                                                                                           OSJNBa0033H08.2 protein.
OSJNBA0033H08.2.
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
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CAE019978

AC CAE0

AC CAE0

DT 02-M

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                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; "Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                      Length 1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
Vibri TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.6%; Score 56; DB 2; Length 422; 35.9%; Pred. No. 22; ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AD005347; FATP binding; IEA.

R GO; GO:000524; F:ATP binding; IEA.

GO; GO:000431; F:RATP binding; IEA.

GO; GO:0004831; F:RATP binding; IEA.

GO; GO:0004831; F:RYCosine-tRNA ligase activity; IEA.

R GO; GO:0004831; F:RYCosyl-tRNA aminoacylation; IEA.

R GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; IEA.

R InterPro; IPRO02305; ENNA-synt_1b.

R InterPro; IPRO01412; ENNA-synt_1b.

R Péan; PPO1479; A4; 11.

R Pfan; PPO1479; A4; 11.

R PROSITE; PS01040; TRNA-SYNTHYR.

R TICRFAM; TIGRO034; tyrS; 1.

R PROSITE; PS01040; TRNA-LIGASE_I; 1.

R PROSITE; PS0889; S4; 1.

R Aminoacyl-tRNA synthetase.

S EQUENCE 422 AA; 47161 MW; OAC47AC4DBA654F5 CRC64;
                                                                                                             10; Indels
OBODE550A15A746E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tyrosyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 IAQTIDLEQLIALFRQPQTLYCGFDPTAGSLHIGHLVPL
                                                         DB 2;
                                                                                                                                                                                                                                584 BORRLLARIPRIPGRLYMLDINLARPVCLAAH 615
                                                                                                                                                                      10 EMEMLLARFRRTPG----DLHLDHSVHLCAH 36
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                                                      27.8%; Score 56.5; D
46.9%; Pred. No. 94;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        422
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QBRYX8;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.5%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAC and BAC clones.";
DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura Y.;
                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                       Q9LH89
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ID Q8
AC Q8
DT 01
DT 01
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DNA Res. 9:121-130(2002)

Li SINILARITY: Belongs to the ABC transporter family.

EMBL; AP005375; BAC09554.1; -..

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:ATP binding; Lassette (ABC) transporter acti. . .; IEA.

GO; GO:0015112; F:nitrate transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BP-1,
MEDLINE=22225144; PubMed=12240834;
MAZBLINE=22225144; PubMed=12240834;
MAZBRINE=22225144; PubMed=12240834;
MAZBRINE=2225144; PubMed=12240834;
MAZBRINE T., Kishida Y.,
Kiyokawa C., Kohara M., MazBRING M., Matsuno A., Nakazaki N.,
Shimpo S., Sugimoro M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                      Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                   "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016811; AAO07799.1; -
                                                                                                                                                                                                                                                                                                                                                                                                      Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 422 AA; 47173 MW; 0C65F0586119F26B CRC64;
                                                                                                                                                                                                                    GO; GO:0005524; F:ATP binding; IBA.
GO; GO:0005523; F:RNB binding; IBA.
GO; GO:0003723; F:RNB binding; IBA.
GO; GO:0006431; F:tyrosine-tRNA ligase activity; IBA.
GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; IBA.
InterPro; IPR002942; S4.
InterPro; IPR002305; FRNA-synt_lb.
InterPro; IPR00412; tRNA-synt_ll.
InterPro; IPR00412; TYT_TRNA-Synt_lb.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Bicarbonate transport system APP-binding protein.
Name=cmpC; OrderedLocusNames=tlr2002;
 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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35.9%; Pred. No. 22;
rative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                      Pfam; PF00579; tRNA-synt lb; 1.
PRINTS; PRO1040; TRNASYNTHYTR.
TIGRPAMS; TIGR00234; tyrS; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
PROSITE; PS50889; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
01-MAR-2003 (TrEMBLrel. 23,
01-07-2003 (TrEMBLrel. 25,
Tyrosyl-tRNA synthetase.
OrderedLocusNames=VV20878;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 35.9'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Pfam; PF01479; S4; 1.
Pfam; PF00579; tRNA-s-
                                                                                                                                                                                                           P00952; 2TS1.
                                                     Vibrio vulnificus.
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=32046;
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                                                                                                                                STRAIN=CMCP6
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Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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EMBL; AP002057; BAB03183.1; -
GO; GO:0005189; F:electron transporter activity; IEA.
GO; GO:0006189; F:electron transport; IEA.
InterPro; IPR00199; ATPASE a/bcentre.
InterPro; IPR00199; Glutaredoxin.
PFGm; FS00152; ATPASE ALPHA, BETA; UNKNOWN 1.
SEQUENCE 428 AA; 48178 MW; IABA2EB141DCAĞEZ CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 27.6%; Score 56; DB 2; Length 658; Local Similarity 41.4%; Pred. No. 37; and 12; Conservative 3; Mismatches 14; Indels
R GO; GO:0000166; F:nucleotide binding; IEA.
R GO; GO:0015706; P:nitrate transport; IEA.
R GO; GO:0016810; P:transport; IEA.
R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR003439; ABC transporter.
R PFOUNDS, ABC transporter.
R PFOUNDS, ABC transporter.
R PROMO182; AAA i.
R TIGREAMS, TIGRO184; ntrCD; 1.
R TIGREAMS; TIGRO184; ntrCD; 1.
R PROSITE; PS00211; ABC TRANSPORTER 1; 1.
R PROSITE; PS00211; ABC TRANSPORTER 2; 1.
R PROSITE; COMplete proteome.
SEQUENCE 658 AA; 72899 MW; AE985AA75901BBE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WIEMDTEME-----MLLARFRRTPGDLHLDHSVHLCAH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 26, Last annotation update)
Emb[CAB72177.1.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AA.
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SEQUENCE FROM N.A.
MEDLINE=20363099; PubMed=10907853;
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Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tenebrio molitor (Yellow mealworm)
EMBL; Z48809; CAA88473.1; JOINED.
PIR, T22615; T22615.
WormPep; T01E8.5; CE18165.
Hypothetical procein.
SEQUENCE 1270 AA; 147634 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X66455; CAA42985.1; -. EMBL; X72783; CAA51290.1; -. PIR; S16663; 516663. PIR; S32224; S32224.
                                                                                                                                                                   27.3%;
Local Similarity 41.9%;
hes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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AC22 TENMO
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Matches
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Mature 420:312-346(2002).
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73
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
        01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
04048009.22 protein (P06988410.19 protein).
Name=P0648009.22; Symonyms=P0698410.19;
Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Sasaki T'., Matsumoto T., Yamamoto K.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA; 64866 MW; 15D366ECBE93F5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein T01E8.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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43.8%; Pred. No. 37;
tive 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEMDTEMEMLLARFRRTPGDLHLDHSVHLCAH 36
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MEDLINE=99069613; PubMed=9851916;
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EMBL; Z48809; CAA88749.1; -.
EMBL; Z48583; CAA88473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP003922; BAB86233.1; -. EMBL; AP003297; BAB92449.1; -.
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investigating biology.";
Science 282:2012-2018(1998)
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Caenorhabditis elegans.
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q20749 PRE
Q20749; Q22073;
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Matches

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RESULT 12

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97242547; PubMed=9087546;
Bouhin H., Braquart C., Charles J.-P., Quennedey B., Delachambre J.;
"Mucleoride sequence of an adult-specific cuticular protein gene from the beetle Tenebrio molitor: effects of 20-hydroxyecdysone on mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adult-specific cuticular protein ACP-22.
Poly-Gly.
Poly-Gly.
Poly-Gly.
Poly-Gly.
S-y (in Ref. 2).
                                                                                                                   Gaps
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Neoptera, Endopterygota, Coleoptera, Polyphaga, Cucujiformia,
Tenebrionidae, Tenebrio.
                                                         Length 1270;
                                                                                                                   Indels
MW; DCB661227D75F541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adult-specific cuticular protein ACP-22 precursor. Name=ACP22;
                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                  AC22_TENMO STANDARD; PRT; 199 AA. P26968; Q27015; 01-AUG-1992 (Rel. 23, Created) OL-LUG-1992 (Rel. 23, Last sequence update) O5-JUL-2004 (Rel. 44, Last annotation update)
                                                         DB
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626 ISWIEVEREMMNIDARVKRIKLKDCELYEDH 656
                                                                                                                                                                                                                                                                                                                                                                                               199 AA
                                                                                                                                                                             2 LSWIEMDTEMEMLLARFRRT---PGDLHLDH 29
                                                         Score 55.5; 1
Pred. No. 94;
                                                                                                                   7; Mismatches
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Zymomonas mobilis.
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                                                                                                                                                                   NCBI_TaxID=542;
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GO; GO:000562; C:intracellular; IEA.
GO; GO:000116; F:transcription factor activity; IEA.
GO; GO:000116; F:two-component response regulator activity; IEA.
GO; GO:000160; F:two-component signal transduction system (p. . .; IEA.
InterPro; IPR010092; HTH_LuxR.
InterPro; IPR001789; Response_reg.
Pfam; PF00196; GerE; I.
Pfam; PF00196; GerE; I.
Pfam; PF00178; Response_reg. I.
                                                                          Gaps
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Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Charaguez-Palenzuela P., Rojas C.M., Alfano J.R., Collmer A., Collmer A.; Collmer A.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                   Length 199;
                                                                        4; Indels
20710 MW; 1EBF2D1DBEC6739F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation.
SEQUENCE 213 AA; 23772 MW; 728465D54BEB4249 CRC64;
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ProDom; PD000307; HTH LUXE; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00421; HTH LUXE; 1.
SMART; SM00448; REC; 1.
PROSITE; PS00622; HTH LUXE FAMILY; 1.
PROSITE; PS0100; RESPONSE REGULATORY; 1.
DNA-binding; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                 27.1%; Score 55; DB 1; 52.9%; Pred. No. 13; ative 4; Mismatches
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                                                                                                                                                                                                                                          PRT;
                                                                                                                                  || |:| :::|| |||
118 TPVDVHHEEAIHLKAHP 134
                                                                                                            21 TPGDLHLDHSVHLCAHP 37
                                                                      Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Erwinia chrysanthemi
199 AA;
                                                       Best Local Similarity
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Best Local Similarity
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SEQUENCE
                                   Query Match
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ID ISDE_ZY
AC Q9RNZI,
DI 16-OCT-
DI 16-OCT-
DT 05-JUL
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Q8KUM3
                                                                        Matches
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Matches
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FT CONFLICT 36 36 N -> I (in Ref. 2).

FT CONFLICT 63 63 T -> A (in Ref. 2).

SQ SEQUENCE 387 AA, 41946 MW; A995805EF9552B27 CRC64;

Query Match

Query Match

26.8%; Score 54.5, DB 1; Length 387;

Best Local Similarity 30.3%; Pred. No. 34;

Matches 10; Conservative 13; Mismatches 9; Indels 1; Gaps

Qy 6 EMDTEMEMILARFRRTPGDLHLDHSV-HLCAHP 37

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DD 16 QVNVQVKALQKQYRKTAGKANLAHP 48
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Search completed: November 10, 2004, 13:38:33 Job time : 47.1796 secs

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5, Appli 42251, A 12, Appl 15, Appl 7410, Ap 12, Appl 12, Appl 1832, Ap 27234, Ap

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US-09-270-767-45056
US-09-270-767-45056
US-09-270-767-45056
Sequence 45056, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62817
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 45056
LENGTH: 265
                                                                                                                                                                Sequence 3991
Sequence 4533
Sequence 3, 7
Sequence 3, 7
                                                          Sequence Sequence Sequence S
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Sequence 2
Sequence 3
Sequence 3
Sequence 3
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Sequence
Sequence
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Pred. No. 7.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                         Sequence 5801, Application US/09621976

Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOBERT, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054 PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NOS 5801
FUND 5801
US-09-252-991A-31560

US-08-714-12-5

US-08-735-89-5

US-08-270-767-42251

US-08-867-0878-17

US-08-867-0878-17

US-08-867-12

US-09-543-681A-7410

US-09-543-681A-7410

US-09-98-12

US-09-98-12

US-09-98-12

US-09-199-63-74-321

US-09-199-63-74-321

US-09-199-63-74-31

US-09-134-001C-3991

US-09-134-001C-3991

US-08-134-01C-3991

US-08-134-01C-3991

US-08-134-01C-3991

US-08-134-01C-3991

US-08-134-01C-3991

US-08-144-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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   ; LOCATION: -46..-1
US-09-621-976-5801
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LOCATION: -46..-1
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Sequence 18, Appl
Sequence 18, Appl
Sequence 57530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2116, Ap
Sequence 4074, Ap
Sequence 4074, Ap
Sequence 1156, A
Sequence 1253, A
Sequence 1253, A
Sequence 1253, A
Sequence 1350, A
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
                                                                                    November 10, 2004, 12:32:37; Search time 3.79965 Seconds (without alignments) 191.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                               isued Patents AA:*
  /cgT2 6/ptodate/1/iaa/5A_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/5B_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/6A_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/6B_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/PoTUS_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/PoTUS_COMB.pep:*
  /cgT2 6/ptodate/1/iaa/PoTUS_COMB.pep:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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-09-270-767-57530
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               protein search, using sw model
                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                 US-10-092-750-34
57
1 TSTLPHIRRTR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                             Copyright
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Match
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Perfect score:
                                                                                                                                                                                Scoring table:
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                                                                protein -
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                   Searched:
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No.
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Gaps

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STREET: 405 Lexington Avenue
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jensen, Einer B.
APPLICANT: Cherry, Joel
APPLICANT: Elrod, Susan L.
TILLE OF INVENTION: Methods For Producing Polypeptides
TITLE OF INVENTION: In Respiratory-Deficient Cells
NUMBER OF SECURNCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,458A
FILING DATE: 17-MAR.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J.
REGISTRATION NUMBER: 33,728
REPERENCE/DOCKET NUMBER: 5215.000-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
                                                                                      Sequence 16, Application US/08819458A
Patent No. 5891669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 8, Conservative
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US-08-819-458A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 405 Le>
                                 RESULT 5
US-08-819-458A-16
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APPLICANT: LYND BOUGETE-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Mucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOLODA
CURRENT PAPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ## PREEDT NO. 00.000010;
## GENERAL INFORMATION:
## APPLICANT: Ratiff, Timothy
## TITLE OF INVENTION: METHOD FOR INHIBITING INFLAMMATORY RESPONSES
## FILE REFERENCE: 140:0010 0101
## CURRENT APPLICATION NUMBER: US 60/121,177
## PRIOR APPLICATION NUMBER: US 60/121,177
## PRIOR APPLICATION NUMBER: 1999-02-22
## NUMBER OF SEQ ID NOS: ## SOFTWARE: PATENTIN Version 3.0
## SEQ ID NO 5
## LENGTH: 381
## TYPE: PRT
## TYPE:
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                                                           Score 36; DB 4; Length 265; Pred. No. 43; 2; Indels
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US-09-583-110-4701
Sequence 4701, Application US/09583110
; Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09510031A
Patent No. 6638518
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                                                           63.2%;
                                                     Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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US-09-270-767-45056
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TYPE: PRT
ORGANISM: Adenovirus
US-09-758-008-4
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Matches 7; Conserv
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STATE: CA
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                                                                                                                                                                                                                                                                                   LENGTH: 362
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0
                                      61.4%; Score 35; DB 4; Length 325; 63.6%; Pred. No. 82; ive 2; Mismatches 2; Indels
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Pred. No. 92;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                      Sequence 3, Application US/09393627B

Pacquence 3, Application US/09393627B

Patent No. 6453144

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

APPLICANT: Wockedi, Imre

APPLICANT: Bruder, Joseph T.

TILLE OF INVENTION: Alternatively Targeted Adenovirus

FILE REFERENCE: 202345

CURRENT ELLING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US 60/099,851

PRIOR APPLICATION NUMBER: US 60/136,529

PRIOR APPLICATION NUMBER: US 60/136,529

PRIOR PLING DATE: 1999-06-28

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 3

SEQ ID NO 3

LENGTH NO 3

LENGTH NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-758-008-2
; Sequence 2, Application US/09758008
; Sequent No. 6635466
; GENERAL INFORMATION:
; APPLICANT: Law, Lane K.
; TITLE OF INVENTION: Adenovirus serotype 30 (Ad30)
; FILE REFERENCE: 875.044USI
; CURRENT APPLICATION NUMBER: US/09/758,008
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2:
; LENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human adenovirus serotype 9
US-09-393-6278-3
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70.0%;
                   Query Match
Best Local Similarity 63.00
The Translative
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Best Local Similarity 70.0
Matches 7; Conservative
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273 SSTLPALRRRR 283
                                                                                                                       1 TSTLPHIRRTR 11
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ORGANISM: Adenovirus
US-09-758-008-2
US-09-252-991A-22955
                                                                                                                                                                                                                         RESULT 7
US-09-393-627B-3
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BESULT.9

Orner House, 4, Application US/09788008

Parent No. 663546

GENERAL INFORMATION:

APPLICANT: Many late K.
APPLICANT: Many late A.
APPLICANTION: Many lat
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                                                                                                                                                                                           61.4%; Score 35; DB 2; Length 638; 70.0%; Pred. No. 1.7e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SOPPET, DANIEL R
APPLICANT: LOS N.
APPLICANT: ROSEN, CRAIG M
APPLICANT: ROSEN, STEVEN M
APPLICANT: ROBEN, STEVEN M
APPLICANT: ROBEN, STEVEN M
APPLICANT: ROBEN, STEVEN M
APPLICANT: ROBEN, STEVEN M
APPLICANT: ROBENS:
APPLICANT: ROBENS:
ADDRESSEE: CARELLA, BYRNE, BAIN GILFILLAN, CECCHI
ADDRESSEE: STEWART & OLSTEIN
STREET: ROSELAND
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM INFO: File ADDRIVED TO SERVICE TO SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08465976A Patent No. 5869632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08982412; Patent No. 5958729; GENERAL INFORMATION: APPLICANT: LI, YI APPLICANT: LI, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.4%;
Best Local Similarity 80.0%;
Matches 8; Conservative
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amino acid
                                                                                                                                                              Query Match
Best Local Similarity 70.v.
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 STLPPPRRTR 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                 84 TGTLPRIHRT 93
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 205011
US-08-681-151-3
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US-08-982-412-2
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RESULT 13
US-10-101-464A-555

i Sequence 555.4 Application US/10101464A

patent No. 6768A1

i GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: APPLICANTON: and Their Use in the Modification of Plant Cell Signaling
FILES OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILES OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILES PRING DATE: 2002-01-10

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1999-01-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 999

SOCTHARRE: FastSEQ for Windows Version 4.0

SSEQ ID NO SSS

LENTH: 144
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Pred. No. 2.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,412
FILING DATE:
APPLICANT: ROSEN, CRAIG A
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR
WHERE OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                               ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROCKES, ANDERS, A.373
REGISTRATION NUMBER: 36,373
REFRENCE/POCKET NUMBER: PP181PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-86439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.4%;
80.0%;
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; ORGANISM: Eucalyptus grandis
US-10-101-464A-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 884 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-982-412-2
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Best Local Similarity 80.0
Matches 8; Conservative
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STATE: ME
COUNTRY:
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Gaps

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59.6%; Score 34; DB 4; Length 159; 63.6%; Pred. No. 58; cive 2; Mismatches 2; Indels
                            TELEPHONE: (781) 893-8277
INFORMATION FOR SEQ 1D NO: 4074:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...159
SEQUENCE DESCRIPTION: SEQ ID NO: 4074:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 10, 2004, 13:44:06 Job time: 4.79965 secs
              TELECOMMUNICATION INFORMATION:
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                 Parent No. 6551795

GENERAL INFORMATION:
Parent No. 6551795

GENERAL INFORMATION:
APPLICANT:
MAIC J. Rubenfield et al.
APPLICANT:
MAIC J. Rubenfield et al.
APPLICANT:
MAIC J. Rubenfield et al.
APPLICANT:
MAIC J. RUBENFION:
APPLICANTION WINGER:
TITLE OF INVENTION:
APPLICATION WHORER:
CURRENT APPLICATION WHORER:
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE:
1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21166

LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4074, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                    Gaps
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    59.6%; Score 34; DB 4; Length 144; 70.0%; Pred. No. 52; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: 14,1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
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COUNTRY: USA
Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                             1 TSTLPHIRRT 10
                                                                                                                                      26 TSLNPHIRNT 35
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US-09-252-991A-21166
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US-09-107-532A-4074
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ORGANISM:
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Sequence 10497, A Sequence 10491, Ap Sequence 152417, Sequence 152417, Sequence 1540, Ap Sequence 1240, Ap Sequence 3144, Ap Sequence 3144, Ap Sequence 354, App Sequence 354,
                               Sequence 170498,
Sequence 255867,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/10092750
| Publication No. US20030032157A1
| GENERAL INFORMATION:
| APPLICANT: Hammond, Philip W.
| APPLICANT: Alpin, Julia |
| APPLICANT: Wright, Martin C.
| TITLE OF INVENTION: Polypeptides Interactive with BCL-X1 |
| FILE REFERENCE: 50036/050002 |
| CURRENT APPLICATION WHORER: US/10/092,750 |
| CURRENT FILING DATE: 2002-03-07 |
| PRIOR PILING DATE: 2001-03-08 |
| PRIOR FILING DATE: 2001-03-08 |
| NUMBER OF FEQUENCE: 5001-03-08 |
| SEQ ID NOS: 253 |
| SEQ ID NOS: 253 |
| SEQ ID NOS: 4000 |
| TENGRAL IN TARGET OF WINGOWS Version 4.0 |
| SEQ ID NOS 44 |
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| TENGRAL IN TARGE
                                                                                          ALIGNMENTS
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Publication No. US20040031072A1
GENERAL INFORMATION:
  TSTLPHIRRTR 11
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ORGANISM: Homo sapiens
US-10-092-750-34
US-10-424-599-242274
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US-10-092-750-34
  RESULT 2
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Sequence 242274,
Sequence 202505,
Sequence 8110, Ap
Sequence 57404, A
Sequence 46417, A
Sequence 77110, A
Sequence 7210, Ap
Sequence 7210, Ap
Sequence 7454, Ap
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328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             November 10, 2004, 16:36:12 ; Search time 11.8169 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB-POP:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB-POP:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB-POP:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB-POP:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB-POP:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB-POP:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB-POP:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.POP:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.POP:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.POP:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.POP:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.POP:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB-POP:*

14: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*

15: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*

16: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*

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18: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*

19: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*

10: /cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.POP:*
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-424-599-242274
US-10-437-963-26255
US-10-156-761-8110
US-10-424-599-252181
US-10-424-599-252181
US-10-424-599-252181
US-10-767-701-46417
US-10-369-493-42379
US-10-369-493-42379
US-10-369-4988-7654
US-09-864-5085-7454
US-10-437-963-189053
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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57
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Match Length DB
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Sequence 252181, Application US/10424599

Sequence 252181, Application US/2040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yih
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Sequence 57404, Application US/10425114
Sublication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Passka, USC, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
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Pred. No. 67;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT3847_69748C.1.pep
US-10-424-599-252181
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
FILE OLIVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FLIENG DATE: 2001-05-30
PRIOR FLIENG DATE: 2001-05-30
PRIOR FLIENG DATE: 2001-05-30
FRIOR FLIENG DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces avermitilis US-10-156-761-8110
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Best Local Similarity 70...
7, Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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64 TTTLPHLPSTR 74
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275 STTPHLRRAR 284
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Burbauuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 202505
   APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242274
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

86.0%; Score 49; DB 15; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels
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US-10-424-599-242274
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US-10-437-963-202505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 202505, Application US/10437963; Publication No. US20040123343A1 GENERAL INFORMATION:
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Best Local Similarity 72.7
Matches 8; Conservative
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442 TSTVPNIERTR 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max PEATURE:
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APPLICANT:
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Sequence 4205, Application US/10369493

Dublication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Gl
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-10-22

PRIOR PLING DATE: 2000-10-22

PRIOR PLING DATE: 2000-10-216

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-206

PRIOR PRIOR PRIOR DATE: 2000-10-206

PRIOR PRIOR PRIOR DATE: 2000-10-20
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8.210-369-493-22379
; Sequence 22379, Application US/10369493
; Publication No. US20030233675A1
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US-10-369-493-4205
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Matches 8; Conservative
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ORGANISM: Vibrio cholerae
US-10-282-122A-77110
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287 SSTLSHLRRT 296
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413 TSTLDYIRRT 422
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Matches 7; Conser
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US-10-67-701-46417
US-10-67-701-46417
Sequence 46417, Application US/10767701
Publication No. US20040172694A1
Sequence 46417
Publication No. US20040172694A1
Septembra. Invocation.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 176
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: 1044
CURRENT REPRENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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US-10-767-701-46417
                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Clone ID: UC-ZMFLMO17344G01_FLI.pep
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; Sequence 77110, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
         CURRENT FILING DATE: 2003-04-28 WIMPER OF SEQ ID NOS: 73128 SEQ ID NO 57404 LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Maselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Famamoto, Robert
APPLICANT: Family
APPLICANT: Famamoto, Robert
APPLICANT: Famamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 75.0
nes 6; Conservative
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ORGANISM: Sorghum bicolor
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1 TSSLPAIRRT 10
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                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                        US-10-425-114-57404
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Matches
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Gaps ö

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Sequence 189053, Application US/10437963

Sequence 189053, Application US/10437963

Publication No. US20040123343A1

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Pland

TITLE OF INVENTION: Plands and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICANTON NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 189053

LENGTH: 100
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Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242031
LENGTH: 116
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                                                                                                                                                                    64.9%; Score 37; DB 11; Length 70; 75.0%; Pred. No. 46; 1. Length 70; 75.0%; Pred. No. 46; 10 Indels
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US-10-437-963-189053
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Pred. No. 66;
1; Mismatches
SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 6100 LENGTH: 70
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Best Local Similarity 75...
6, Conservative
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Best Local Similarity 70.0.
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ORGANISM: Oryza sativa
                                                                                                 ; ORGANISM: Homo sapiens US-09-864-408A-6100
                                                                                                                                                                                                                                                                                                      30 STLPHLRK 37
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NAME/KEY: unsure
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US-10-424-599-242031
                                                                          TYPE: PRT
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Publication No. US20040009474A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides EncoTITLE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
                 APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gaolman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Gho, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22379
LENGTH: 1224
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Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Reemer D.
APPLICANT: Bo, Jiang
APPLICANT: Howard, Buseey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: 3001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7454
LENGTH: 1234
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
70.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative :
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US-10-032-585-7454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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489 SSTLSHLRRT 498
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484 SSTLSHLRRT 493
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     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-864-408A-6100
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US-10-032-585-7454
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TITE OF INVENTION: Brad With TITE OF INVENTION: Blad Molecules and Other Molecules Associated With TITE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITE OF INVENTION: Plants and Uses Thereof for Plant Improvement; CURRENT APPLICATION WINDERS: US/10/437,963; CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 170498

LENGTH: 208

TYPE: PLANT TITE OF ASSOCIATED AND ASSOCIATED ASSOCIATED AND ASSOCIATED ASSOCI
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Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 87.5%; Pred. No. 77;

Matches 7; Conservative 0; Mismatches 1; Indels
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COCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_68819C.1.pep
US-10-437-963-170498
; LOCATION: (1)..(116)
; OTHER INFORMATION: unsure at all Xaa locations FALTURE:
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60581C.1.pep US-10-424-599-242031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170498, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yihua
    APPLICANT: Cao, Yihua
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Buckharov, Andrey A.
    APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TSTLPHIRRTR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 TLPHIRMT 111
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US-10-437-963-170498
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Search completed: November 11, 2004, 01:28:16 Job time: 12.8669 secs

15 TSTTPRPRRTR 25

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us-10-092-750-34.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 2.45078 Seconds (without alignments) 431.857 Million cell updates/sec on:

Run

US-10-092-750-34 57 1 TSTLPHIRRTR 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein T27A10.6 [i i	DNA-directed RNA p	ш	DNA-directed RNA p	l prot	-4	cal	e e	gamma-1-microglobu	IS1167, transposas	het	ď	protein -	unc-5 protein, lon	conserved hypothet	chaoptin precursor	conserved hypothet	insulin-like prote	fiber protein - hu	fiber protein - hu	hypothetical prote	probable cycA prot	sid	_	plasma kallikrein	glutamate synthase
SUMMARIES	ID	950	269	\mathbf{H}	229	88	997	വ	ß	4,	T44914	T36913	8	C95053	T30645	JQ2205	T32541	B44294	AD0301	A29944	E75546	A38422	S37220	S40092	T25178	G70503	T02402	KOMSPL	ы	T02097
	DB					~																								
	Length	898	42	738	868	1224	383	1210	1879	64	107	314	355	422	772	808	919	947	1095	1134	278	305	362	362	366	556	591	638	638	1137
dР	Query	0	66.7	φ	66.7	66.7	4	4	4	$^{\circ}$	m	'n	m	63.2	m	m	m	m	63.2	m	61.4	61.4			61.4			61.4	61.4	61.4
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T00250 C84839	G69441 T35305	T03041 T20063	T36104	A/US18 C96621	AI3370 E96492	F96502	C71367	F96581	KFHU1
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1364	169	236 318	436	404 474	486 538	570	607	622	625
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30 31	1 C3 E9 1 E9 E9	ພ ຍ 4 ፕ	36	~ 80 m m	39 0.4	4.	4. 4. 7. W	44	45

ALIGNMENTS

RESULT F89500 C) Date	1 T27A10.6 [imported] - Caenorhabotes: Caenorhabditis elegans: 10-May-2001 #sequence_revision. Sesion: F89500 elegans Sequencing (e. 282, 2012-2018, 1998 e. 282, 2012-2018, 1998 e. Genome sequence of the nematod rence number: A75000, MUID:990696; see websites genome wustl.edu/gi: see websites genome wustl.edu/gi: published errata appeared in Scresion: F89500 esion: F99500 cule type: DNA dues: 1-868 <sto> references: UNIPROT:Q22822; GB::1405: 1727A10.6</sto>
Ğ₩ ₩	Query Match 70.2%; Score 40; DB 2; Length 868; Best Local Similarity 72.7%; Pred. No. 17; Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
λ ₀ α ₀	1 TSTLPHIRRTR 11
RESULT PRESULT PRESULT C)Spect	RESULT 2 F82691

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conserved hypothetical protein SA1693 [imported]
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laigr chado, M.A.; Madeira, A.M. Madeira, H.N.F.; Marino, C.L.; Marques, M.V.; Martins, B.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsuhako, M.H.; Vallada, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, R.R.; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. J. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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R;Alm, R.A.; Stroeher, U.H.; Manning, P.A.
Mol. Microbiol. 2, 481-488, 1988
A;Title: Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structura
in the non-haemolytic classical strain 569B.
A;Reference number: S01892; MUID:89013889; PMID:3050359
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A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
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Alterander names: El Tor hemolysin C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
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Pred. No. 34;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2;
Pred. No. 1.8;
1; Mismatches
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illarity 70.0%;
Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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A,Residues: 1-738 <ALM>
A,Cross-references: EMBL:Y00557
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STMPHQHRTR 26
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TNTLPHVR 166
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Best Local Similarity
Matches 7; Conserv
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DNA-directed RNA polymerase (BC 2.7.7.6) II 140K chain [validated] - yeast (Saccharomyces NyAlternate names: DNA-directed RNA polymerase B chain B150; protein 03533; protein YORLE C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C; Accession: A25884; S36660; A37884; S78039
R; Sweetser, D.; Nonet, M.; Young, R.A.
R; Sweetser, D.; Nonet, M.; Young, R.A.
A; Title: Prokaryotic and eukaryotic RNA polymerases have homologous core subunits.
A; Reference number: A25884; MUID:87147239; PMID:3547406
C, Superfamily: translation initiation factor IF-2; translation elongation factor Tu homol F;400-509/Domain: translation elongation factor Tu homology <ETU>
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A;Cross-references: UNIPROT:P08518; EMBL:M15693; NID:g172210; PIDN:AAA68096.1; PID:g17221
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A.Residues: 961-990 «RIV»
R.Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winso:
Submitted to the Protein Sequence Database, July 1996
A.Reference number: S67032
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A.Residues: 1-1224 <BOR>
A.Cross-references: EMBL:Z75059; NID:g1420378; PIDN:CAA99357.1; PID:g1420379; MIPS:YOR151
A.Experimental source: strain S288C
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C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger
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A; Residues: 1-1002, RRRY', 1007-1224 <SW2>
A;Cross-references: EMBL:M15699; NID:9172210; PIDN:AAA68096.1; PID:9172211
R;Riva, M.; Carles, C.; Sentenac, A.; Grachev, M.A.; Mustaev, A.A.; Zaychikov, E.F.
J. Balol. Chem. 265, 16498-16503, 1990
A;Title: Mapping the active site of yeast RNA polymerase B (II).
A;Reference number: A37894; MUID:90375520; PMID:2204624
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Pred. No. 58;
                                                                                                     Score 38; DB 2
Pred. No. 42;
1; Mismatches
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ilarity 70.0%;
Conservative
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ilarity 80.0%;
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 7; Conserv
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- Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

A,Gene: VC0643 A,Map position: 1

us-10-092-750-34.rpr

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A,Molecule type: DNA
A,Residues: 1-1879 <FAV>
A,Cross-references: UNIPRCT:Q19161; EMBL:U46672; NID:g1166599; PID:g1166600; PIDN:AAA857:
C;Genetics:
A;Gene: CESP:P07C7.1
A;Introns: 818/1; 1522/1; 1702/3; 1784/1
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A,Molecule type: DNA
A,Residues: 1-64 <TIGR>
A,Cross-references: UNIPROT: P44021; GB:U32741; GB:L42023; NID:g1573582; PIDN:AAC22259.1;
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hypothetical protein HI0592 - Haemophilus influenzae (strain Rd KW20)
c)Species: Haemophilus influenzae
c)Species: Haemophilus influenzae
c)Species: Haemophilus influenzae
c)Accession: C64010
C)Acces
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R;Parkhill, J; Barrell, B.G; Rajandream, M.A. submitted to the EMBL Data Library, August 1997
A;Reference number: Z22864
A;Accession: T44914
A;Reference number: Z22864
A;Cossion: T44914
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-107 <PAR>A;Residues: 1-107 <PAR>A;Residues: 1-107 <PAR>A;Residues: 1-107 <PAR>A;Residues: C;Genetics: C;Genetics: A;Note: MLCB22.49
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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87.5%;
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Best Local Similarity 8/...
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Best Local Similarity 70.0
Matches 7; Conservative
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54 TSSMPEVRRRR 64
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Best Local Similarity
Matches 6; Conserv
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T36913
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835548
DNA-directed RNA polymerase (EC 2.7.7.6) II chain 2 - fission yeast (Schizosaccharomyces C; Species: Schizosaccharomyces pombe
C; Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C; Accession: 355548
R; Kawaqishi, M.; Yamagishi, M.; Ishihama, A.
Nucleic Acids Res. 21 46-473, 1993
Nucleic Acids Res. 21 46-473, 1993
Nucleic Acids Res. 21 46-473, 1993
A; Title: Cloning and sequence determination of the Schizosaccharomyces pombe rpb2 gene e
A; Reference number: 335548; MUID:93181236; PMID:8441660
A; Accession: 335548
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Status: nucleic acid sequence was confirmed by mRNA sequencing
R; Kawaqishi: Kobayashi, M.; Yamamoto, M.; Ishihama, A.
A; Cross-references: UNIPROT:Q02061; EMBL:D13337; NID:9218553; PIDN:BAA02600.1; PID:92185
A; Note: part of this sequence was confirmed by mRNA sequencing
R; Kawaqishi: Kobayashi, M.; Yamamoto, M.; Ishihama, A.
A; Crotent: annotational analysis of the RNase-like domain in subunit 2 of fission yeast RNA
A; Contents: annotation; mutational analysis
C; Genetics:
A; Chenerics:
A; Ch
C; Accession: D89975

B; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguda, M.; Aizutani Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A; Reference number: A89758; MUD:21311952; PMID:11418146

A; Accession: D89975

A; Residues: 1-383 < KUR>
A; Residues: 1-383 < KUR>
A; Cross-references: UNIPROT:Q99704; GB:BA000018; PID:g13701670; PIDN:BAB42963.1; GSPDB:GGGenetics:
A; Cene: SA1693
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T15962
T15962
C)Potest Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C)Accession; T15962
By Fravello, T.
Submitted to the EMBL Data Library, January 1996
A)Description: The sequence of C. elegans cosmid F07C7.
A)Reference number: 218437
A)Accession: T15962
A)Accession: T15962
A)Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 89;
1; Mismatches 1; Indels
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Pred. No. 27;
2; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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195 STLPHLRK 202
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A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host res
A;Reference number: Z20876; MUID:96325459; PMID:8670425
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A,Residues: 1-808 cYAN-
A,Cross-references: UNIRROT:Q69320; GB:L10283; NID:g388703; PIDN:AAA03150.1; PID:g388708
A,Experimental source: strain GA
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R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss,
Science 273, 813-816, 1996
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Cispecies: Marek's disease virus
Cispate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Ciscossion: 02205
Riyangdida, N.; Yoshida, S.; Nazerian, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A;Title: Nucleotide and predicted amino acid sequences of Marek's disease visite ference number: 02199; MUID:93389438; PMID:8397281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                     Gaps
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A;Note: MC043L
C;Superfamily: Molluscum contagiosum virus 1 hypothetical protein 43L
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                                                                                                                                                Query Match 63.2%; Score 36; DB 2; Length 422; Best Local Similarity 75.0%; Pred. No. 46; Astches 6; Conservative 1; Mismatches 1; Indels
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                                      A;Gene: SP0460
C;Superfamily: Lactobacillus delbrueckii ISL3 transposase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 43L - Molluscum contagiosum virus 1 N/Alternate names: MCO43L
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ilarity 70.0%; Pred. No. 86;
Conservative 0; Mismatches 3
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Best Local Similarity 62.5%; Pred. No. 90;
Matches 5; Conservative 3; Mismatches C
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UL47h protein - Marek's disease virus
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Best Local Similarity
7; Conserva
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    C; Genetics
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95653
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
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A;Stetus: preliminary
A;Rolecule type: DNA
A;Residus: 1-422 «KUR»
A;Residus: 1-422 «KUR»
A;Cross-references: UNIPROT:0978CS; GB:AE005672; PIDN:AAK74620.1; PID:g14971930; GSPDB:G
A;Cross-references: triain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-314 <SEE>
A;Cross-references: UNIPROT:09X9X3; EMBL:AL096743; PIDN:CAB46400.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
                                                                                                                       C;Accession: T36913 ... R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
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probable integral membrane sugar transport protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Pleuronectes platessa (plaice)
C;Accession: S22181
R;Leaver, M.J
submitted to the EMBL Data Library, December 1991
A;Reference number: S22181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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85.7%; Pred. No. 34;
tive 1; Mismatches 0; Indels
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Best Local Similarity 85.,
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                                                                                                                                                                                                                                              A;Reference number: Z21574
A;Accession: T36913
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TLPHLRR 231
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A;Molecule type: mRNA
A;Residues: 1-355 <LEA>
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Query Match Best Loc Matches

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RESULT 12

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November 10, 2004, 12:27:34; Search time 13.4318 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-092-750-34 57 1 TSTLPHIRRTR 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1 093136	ID 093136 PRELIMINARY; PRT; 615 AA.	01-DEC-2001 (TrEMBLrel. 19, Creat	ol-OCT-2004 (Inchesting) 15, mast 01-OCT-2003 (TEMBLE) 25, Last Unotherical archaelast	nrecinetical Florein. Rhisobium leguminosarum (biovar viciae). Bacteria: Drotechacteria: blohamotechacteria.	Rhizobiaceae, Rhizobium/Agrobacterium group; Rh				MEDLINE=99113394; FubMed=9914965; Sadvkov M.R., Ivashina T.V., Kanabin A.A.,	Ksenzenko V.N.;	"Structure-functional organization of exopolysaccharide	genes in Rhizobium Leguminosarum bv. viciae VF39			STRAIN=VE39;	Druzhinina I.V., Sauykov M.K., Kalinchuk M.R., Senchenkova Druzhinina T.N., Grachev A.A., Shashkov A.S., Shibaev V.N	Kanapin A.A., Shlyapnikov M.G.,	Ksenzenko V.N.;	Submitted (JUL-2001) to the RMRI, AF028810, AAK77321.1;	InterPro; IPR001440;	InterPro; IPR008941; I	FROSLIE; FSSUZUS; TPR	Hypotnetical SEQUENCE 61	atch cal Similarity 88.9%; Pred. No. 15;	vative 0; Mismatches 1; Indels 0;	Qy 3 TUPHIRPTR 11	Db 389 TLPHIRRAR 397	RESULT 2 OACG25	ID QCCG25 PRELIMINARY; PRT; 465 AA.	01-0CT-2004 (TremBirel. 28, Created) 01-0CT-2004 (TremBirel. 28) Last sequence up	01-001-2004 (IIEMBLIEL: 28, DASC AMMOCACION	しょうしょく しょうしょく コンフィー しょうしょう りょうしん	RESULTANDO CO	11. 12. 13.136 PRELIMINARY; PRT; 615 AA. 13.136, 1-DEC-2001 (TrEMBLrel. 19, Last sequence upde l-DEC-2003 (TrEMBLrel. 15, Last annotation upde cotestical protein. 15, Last annotation upde detection protein. 15, Last annotation upde cotestical protein. 25, Last annotation upde cotestical cotestical protein. 25, Last annotation upde cotestical cotestical and cotestical and cotestical cotestical and cotestical annotation updeced. 28, Last annotation updeced. 28, Last annotation updeced. 2001.
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PubMed=15070748;
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Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
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PubMed=15070748;
Liu Y.J., Hall B.D.,
"Body plan evolution of ascomycetes, as inferred from an RNA
"Body plan evolution of ascomycetes, as inferred from an RNA
ploymerase II phylogeny.",
Proc. Natl. Acad. Sci. U.S.A. 101:4507-4512 (2004).
ORFNames=YALIOBO1452g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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InterPro; IPR007421; RNA_pol_B.
InterPro; IPR007642; RNA_pol_Rpb2_2.
InterPro; IPR007645; RNA_pol_Rpb2_2.
InterPro; IPR007645; RNA_pol_Rpb2_3.
InterPro; IPR007646; RNA_pol_Rpb2_4.
InterPro; IPR007646; RNA_pol_Rpb2_4.
InterPro; IPR007646; RNA_pol_Rpb2_6.
InterPro; IPR007610; RNA_pol_Rpb2_6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR302128; CAG82604.1; -
SEQUENCE 465 AA; 52869 WW; 1D56E4BE4CBEBC88 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DNA-dependent RNA polymerase II second largest subunit
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"Genome evolution in yeasts.";
Nature 430:35-44(2004).
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Best Local Similarity 63.6
Matches 7; Conservative
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174 TSSIPHVRFTR 184
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                                                                                              NCBI_TaxID=4952;
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Eukaryota, Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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80.0%; Pred. No. 46;
ative 1; Mismatches 1; Indels
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DR Pfam; PF04563; RNA pol Rpb2_1; 1.

DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.

DR Pfam; PF044565; RNA_pol_Rpb2_3; 1.

DR Pfam; PF04565; RNA_pol_Rpb2_4; 1.

DR Pfam; PF004567; RNA_pol_Rpb2_5; 1.

DR Pfam; PF00562; RNA_pol_Rpb2_5; 1.

DR PROSITE; PS01166; RNA_pol_BETA; 1.

W DNA-directed RNA polymerase; Transcription; Transferase.

T NON_TER 1114 1114 AA; 195495 A.
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"Body plan evolution of ascomycetes, as inferred from an polymerase II phylogeny.";
proc. Natl. Acad. Sci. U.S.A. 101:4507-4512(2004).
EMBL; AY485620; AAS67509.1; -.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; APO05167; BACG3803.1; -
InterPro; IPR008997; RicinB_like.
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14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DNA-dependent RNA polymerase II second largest subunit
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative r40c1 protein.
Name=05JNBa0060017.9;
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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";
Nat. Biotechnol. 21:256-531 (2003).
BENBL, APOD5023; BAC68278.1; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005549; F:ATP binding; IEA.
InterPro; IPR001934; ATPhind ATPase.
InterPro; IPR001932; PP2C-like.
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01-NRR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-OCT-2003 (TrEMBLRel. 25, Last an
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                           Pfam; PF02518; HATPase_c; 1.
SWART; SW00387; HATPase_c; 1.
SWART; SW0031; PP2C_SIG; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 339 AA; 36011 MW; 0D3A5258234F898F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; US8734; AABS2504.3; --
PIR; F89500; F89500.
Wormbep; T27Al0.6; CE30193.
Hypotherical protein.
SEQUENCE 870 AA; 98207 WW; B3AC8105E0308A45 CRC64;
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
         Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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275 STTPHLRRAR 284
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Matches 7; Conserv
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Q22822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzes, Oryza, Oryza sativa.
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MEDLINE=21477403; PubNed=11572948;
MEDLINE=21477403; PubNed=11572948;
Omuta S., Ikeda H., Ibikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilisg deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 23;
2; Mismatches 2; Indels
                                                          71.9%; Score 41; DB 2; Length 402; 63.6%; Pred. No. 23; ive 2; Mismatches 2; Indels
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EMBL; AP005167; BAC83803.1; -. SEQUENCE 402 AA; 44455 MW; 667C4859F72E7589 CRC64;
402 AA; 44455 MW; 667C4B59F72E7589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                       402 AA
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                          BAC83803,
02-WAR-2004 (TrEMBLrel. 27, C1
02-WAR-2004 (TrEMBLrel. 27, L6
02-WAR-2004 (TrEMBLrel. 27, L6
Putative r40cl protein.
OSJNBA0060017.9.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
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Best Local Similarity 63.6
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                                                                                    Local Similarity 63.63.68
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   SEQUENCE
                                                          Query Match
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Phosphorylation; Receptor; Sensory transduction.
SEQUENCE 762 AA; 85320 MW; F9071592179EA3CE CRC64;
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Q9XJ17
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Q9PDM8
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SEQUENCE FROM N.A.
MEDLINE_22149310; PubMed=12154144;
Xie C., Zhang Z.G., Zhang J.S., He X.J., Cao W.H., He S.J., Chen S.Y.;
Xie and Characterization of a putative ethylene
"Spatial expression and characterization of a putative ethylene
receptor protein NTHX1 in tobacco.";
Plant Cell Physiol. 43:810-815(2002).
                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPUENCE FROM N.A.

Zhang J.-S., Xie C., Liu F., Liu F., Chen S.-Y.;

Zhang J.-S., Xie C., Liu F., Liu F., Chen S.-Y.;

"A novel tobacco gene coding for a product similar to bacterial two-component regulators.";

Chin. Sci. Bull. 44:1025-1029(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
Zhang J.S., Xie C., Shen Y.G., Chen S.Y.;
A two-component gene (NTHK1) encoding a putative ethylene receptor homolog is both developmentally and stress-regulated in tobacco.";
Theor. Appl. Genet. 102:815-824(2001).
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Plant J. 33:385-393(2003).
-1- SIMILARITY: Contains 1 histidine kinase domain.
EMBL, APCS26267, ASC31213.3;
-1- SIMILARITY: TO 1930.
HSSP, P49333; IDCF.
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MEDLINE=22444050; PubMed=12535351;
Xie C., Zhang J.S., Zhou H.L., Li J., Zhang Z.G., Wang D.W.,
Chen S.Y.,
                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Ethylene receptor homolog.
Name-NTHK1;
                                                                                                                           762 AA.
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SMART; SM00387; HATBASE c; 1.
SMART; SM00388; HISKA; 1.
PROSTIE; PS50110; HIS KIN; 1.
PROSTIE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                           PRT;
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Pfam; PF00072; Response_reg; 1.
ProDom; PD000039; Response_reg;
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Simpson A.JG. Reinach F.C., Arruda P., Abreu F.A., Acencio M., Simpson A.JG. Reinach F.C., Arruda D., Bati G.S., Baptista C.S., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Alvascorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Commargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colone G., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Farga G.S., Farnes S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ryiner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                          0.-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
0ryza sativa (japonica cultivar-group).
0ryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrharcoideae, Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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                             2; Length 762;
                             68.4%; Score 39; DB 2; Length 762
72.7%; Pred. No. 1.2e+02;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Nagamura Y., Yamamoto K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO0348421, BAA78735.1; -.
Gramene; Q9XJ17; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyporhetical protein.
SEQUENCE 201 AA; 21230 MW; DDE198727729540B CRC64;
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Last annotation update)
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56.2%; Pred. No. 32;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:|||
97 TATVPHIGRAVPRRTR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.2*
Conservative
9, Conservative
Query Match
Best Local Similarity 72...
8; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                554 TSTLPHCCETR 564
                                                                                                                                         1 TSTLPHIRRTR 11
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Gaps

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AgCP5849 (Fragment).

Name=agCG22391; ORFNames=ENSANGG0000018149;

Anopheles gamtiae str. PEST.

EURATYOCA; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

NCBI_TaxID=180454;
                                                                                                                       STRAIN=CBS 2285;
Jeznann S., Cox C.J., Schoenian G., Vilgalys R.J., Mitchell T.G., molecular Phylogeny and Evolution of Candida and Related Species Within the Order Saccharomycetales as Inferred From Multilocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Nectria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 38; DB 2; Length 129; 70.0%; Pred. No. 25; 1; Indels cive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                     Sequence Analysis.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY497608; AAT12528.1; -.
NON TER 129 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 AA; 14706 MW; 82AECOB1D7D28326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RNA polymerase II subunit (Fragment).
Name=RRB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AA.
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EMBL; AAAB01008960; EAA11578.1; -.
NON TER
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les 7; Conservative
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86 SSTLSHLRRT 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nectria cinnabarina
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                                                                                    SEQUENCE FROM N.A.
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           NCBI_TaxID=28549;
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Q7Q5V1;
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Matches
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Q7Q5V1
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Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
A Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagal M.A., Nascimento A.L.T.O., Netro L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.W., Pereira G.A.G., Pereira D.A., Pergero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E., Tr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., da Silva A.M., de Souza A.D.,
A de Souza A.D., Terentzi M.L.Z., Siqueira W.J., Tsuhako M.H.,
Vallada H., Van Sluys M.A., Verlovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
The genome sequence of the plant pathogen Xylella fastidiosa.";
REMBL, AE003967; AAF84160.1; -.
EMBL, RE0591: F82691: F82691: F82691: F82691: F82691: F82691: R2000).
W. Complete proteome; Hypothetical protein.
SEQUENCE 42 AA; 4915 MW; 0F9B51F876FE0C9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Discramn S., Cox C.J., Schoenian G., Vilgalys R.J., Mitchell T.G.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX497608; AAT12528.1; -.
EINTERPERS, IRROY645; RNA_DOl_Rpb2_3.
Pfam, PF04565; RNA_DOl_Rpb2_3.
NON_TER
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Saccharomycetales; Saccharomycetaceae; Debaryomyces.
NCBI_TaxID=28549;
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20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
RMA polymerase II second largest subunit (Fragment).
Bebaryomyces carsonii.
Bukaryota, Fundi; Ascomycota; Saccharomycetina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RNA polymerase II second largest subunit (Fragment)
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STMPHQHRTR 26
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Best Local Similarity
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SEQUENCE
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Облена;
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060 TH8
1D 060 EH
NC 060 EH
DT 05-JU
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Gaps

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AAT12528
ID AAT1
AC AAT1
DT 20-M
DT 20-M
DT 20-M
OC EUKA

d

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Chaverri P., Castlebury L.A., Overton B.E., Samuels G.J.;

Thypocrea/Trichoderma: species with conidiophore elongations and green ondida."

Mycologia 95:1100-1140(2003).

EMBL, AF645567, AAQ11957.1;

InterPro; IPR007645; RNA_pol_Rpb2_4.

InterPro; IPR007645; RNA_pol_Rpb2_4.

InterPro; IPR007645; RNA_pol_Rpb2_4.

InterPro; IPR007647; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5.

Pfam; PF04565; RNA_pol_Rpb2_5; 1.

Pfam; PF04567; RNA_pol_Rpb2_5; 1.

Pfam; PF04667; RNA_pol_Rpb2_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
66.7%; Score 38; DB 2; Length 301;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 2; Mismatches 1; Indels
                             RATA BELLA B
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0; Gaps

Search completed: November 10, 2004, 13:38:34 Job time : 14.4318 secs

1 TSTLPHIRRT 10 :||| |:||| 24 SSTLSHLRRT 33

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9; Conservative
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TOPOLOGY: linear
US-09-097-889-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
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Sequence 1954, A
Sequence 15, Appl
Sequence 1337, A
Sequence 61086, A
Sequence 61086, A
Sequence 61086, A
Sequence 64, Appl
Sequence 18, Appl
                                                                                                                                                                                                        November 10, 2004, 12:32:37; Search time 4.14508 Seconds (without alignments) 191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/8G_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-097-889-18
US-09-097-889-18
US-09-098-079-18
US-08-811-519-25
US-08-811-519-25
US-08-811-519-25
US-08-453-956-15
US-08-453-956-15
US-09-489-093A-13377
US-09-489-093A-13377
US-09-270-767-61086
US-09-270-767-61086
US-09-248-796A-17997
US-09-248-796A-17997
US-09-248-796A-17997
US-09-248-796A-17997
US-09-270-767-6186
US-09-248-796A-17997
US-09-540-256-2570
US-09-540-256-2570
US-09-540-256-2570
US-09-540-256-2570
US-09-540-266-2570
US-09-69-266-2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein, - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                   US-10-092-750-35
60
1 NGNLFASFIADS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
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Gaps

0

Length 226 Indels

DB 3;

70.0%; Score 42; DB 90.0%; Pred. No. 6.3; ive 0; Mismatches

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Sequence 7248, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 25, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 75, Appl
Sequence 750, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTER DETECTABLE MITOCHONDRIAL DNA RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPEICANT: Herrnstadt, Corrina
APPLICANT: Herrnstadt, Corrina
APPLICANT: GASA, Sountra S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE
TITLE OF INVENTION: AGENTS THAT GOANTATIVELY AND METHORS OF THAT OCHONDRIAL DNA: MITOCHONDRIAL DNA: MADDING TO COUNTRY: USB STATE: Washington
COUNTRY: Sastle FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
MEDIUM TYPE: BatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
MEDIUM TYPE: AGENT INPERMATION:
MANE: ROSEMMEN HOPPMATION:
MANE: ROSEMMEN PLO: Stephen J.
REGISTRATION NUMBER: 43,058
REGISTRATION
                               Sequence
US-08-869-477-4
US-09-328-352-7248
US-08-142-39A-2
US-08-143-1603-16
US-08-453-956-25
US-08-453-956-25
US-08-453-956-25
US-09-631-603-17
PCT-US93-08174-25
US-09-631-603-17
US-09-631-603-17
US-09-631-603-17
US-09-631-10-4577
US-09-328-352-7560
5457037-3
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                                                                                                                                                                                                                                                                                                                                                                                                                      5457037-5
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; Sequence 18, Application US/09097889
; Patent No. 6218117
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Gaps

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RESULT 4
US-08-811-519-25
; Sequence 25. Application US/08811519B
; Patent No. 6630345
; Patent No. 6630345
; GENERAL INPORMATION:
; APPLICANT: PETENCK, Alexandre
; TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
; TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
; FILE REFERENCE: 1049-1-007
; CURRENT APPLICANTON NUMBER: US/08/811,519B
; CURRENT FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 4; Length 207;
Pred. No. 13;
2; Mismatches 0; Indels
                                                                                        Score 42; DB 4; Length 404;
Pred. No. 12;
                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SEATTLE
COUNTRY: WA
COUNTRY: WA
ZIP: 99104-7092
COMPUTER READALE FORM:
MEDTION TYPE: COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATTEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,956
FILING DATE: 30-MAY-1995
CLASSIFICATION NUMBER: 08 086,631
FILING DATE: 30-MAY-1995
APPLICATION NUMBER: US 07/938,331
RILING DATE: 28-AUG-1992
ATTONEY/AGENT INFORMATION:
ANALY ACCURATION NUMBER: US 07/938,331
APPLICATION NUMBER: US 07/938,331
APPLICATION NUMBER: DE AUG-1992
ATTONEY/AGENT INFORMATION:
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08453956
Patent No. 577045
GENERAL INPORMATION:
APPLICANT: Kindsvogel, Waylne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McMasters, David D. REGISTRATION NUMBER: 33,963
                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19544
                                                                                                                                                                                                                              219 NGNLFASVSEDS 230
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Best Local Similarity 77.8-
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US-08-453-956-15
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Sequence 19544, Application US/09248796A
Sequence 19544, Application US/09248796A
Sequence 19544, Application US/09248796A
Sequence 19544, Application US/09248796A
Sequence 19544, Application:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PAPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                                                                         Sequence 16, Application US/09098079

Sequence 16, Application US/09098079

REPETON: 6489095

GENERAL INFORMATION:
APPLICANT: Herrhetadt, Corrina
APPLICANT: Clevenger, William
APPLICANT: Fahy, Boin F.
APPLICANT: Pahy, Boin F.
APPLICANT: Davis Boin F.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF TITLE OF INVENTION: EXPRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPEP 81044

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUW-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: ROSENMAN Ph.D., Stephen J.
REGISTRATION NUMBER: 43,088
REPERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NGNLFASFIA 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                    JS-09-098-079-18
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Gaps

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US-08-452-930-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 40; DB 1; Length 485; 77.8%; Pred. No. 33;
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COUNTRY: USA

ZIPE 99104-7092

ZOMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: JN 1, 1993
CLASSIFICATION 1, 1993
CLASSIFICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCMAGLES' DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 39,9008,424C1
TELECOMMUNICATION NUMBER: 39,963
REFERENCE/DOCKET NUMBER: 990008,424C1
TELECOMMUNICATION NUMBER: 30,963
REFERENCE/DOCKET NUMBER: 990008,424C1
TELECOMMUNICATION NUMBER: 30,963
REFERENCE/DOCKET NUMBER: 990008,424C1
TELECOMMUNICATION NUMBER: 990008,424C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-086-631-15
Sequence 15, Application US/08086631
Sequence 15, Application US/08086631
Select No. 5776725
GENERAL INFORMATION:
APPLICANT:
APPLICATION:
CITY:
APPLICATION:
COLUMBIA CENTER
CITY:
APPLICATION:
APPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
REFERENCE/DOCKET NUMBER: 990008.424C1
                                                    TELECOMMUNICATION INFORMATION
TELEPHONE: 206-622-4900
TELEFAX: 206-632-6031
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-453-956-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 HGNLFASFV 186
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Sequence 13, Application US/0845230
GRENEAL INFORMATION:
MILESON SILVEN KILDANOSE, MAYINE R. PRESENCE
COMPENSENT KILDANOSE, MAYINE R. REPROSE
MILITIES OF UNIVERSES:
COMPENSENT SENTINE SENTINE SENTINE
SENTINE SENTINE MASS.
COUNTRY: UNA
SENTINE WAS COLUMBIA CENTER
STREET, 630 COLUMBIA CENTER
STREET, MASS.
COUNTRY: UNA
SENTINE AND SERRY
MANUEL REDABLE PORM: 108, MASS.
MANUEL SENDABLE PORM: 108, MASS.
MANUEL MASS.
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Gaps

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Sequence 17937, Application US/09248796A

Batent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17937
LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parent No. 67034 Application US/09270767

Parent No. 6703491

GRNERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45573

LENGTH: 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.0%; Score 39; DB 4; Length 148; 80.0%; Pred. No. 13; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                     Length 120;
                                                                                                                                                                                                                                                   Score 39; DB 4;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Xaa means any amino acid US-09-270-767-45573
    FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61086
LENGTH: 120
                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-09-270-767-61086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                     65.0%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.v.
8, Conservative
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US-09-248-796A-17937
                                                                                                                                                                                                                                                                                                                                                                             13 NLFAAIIADS 22
                                                                                                                                                                                                                                                                                                                                          3 NLFASFIADS 12
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41 NLFAAIIADS 50
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-270-767-45573
                                                                                                                                                                TYPE: PRT
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Patent No. 6610836
Patent No. 6610810
Patent No. 6610810

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR RAPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13377
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4; Length 116; Pred. No. 10; 2; Mismatches 3; Indels
                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08174
FILING DATE: 30-AUG-1993
CLASSIFICATION:
                                                                                                                                                                     PULBOSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: 010,7 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 990008.424C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 206-622-4900
INFORMATION FOR SEQ ID NO: 15:
LENGTH: 485 amino acids
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.78;
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58.3%;
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amino acid
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 HGNLFASFV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Gaps

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Gaps ;

1; Indels

0; Mismatches

10; Conservative

Matches

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Score 35; DB 4; Length 330;
Pred. No. 1.7e+02;
                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                          Search completed: November 10, 2004, 13:44:07 Job time: 5.14508 secs
                                                                                                                                                 58.3%;
                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2570
LENGTH: 330
                                                                                                                                                                                                                                                                     117 GNSFSSFVRD 126
                                                                TYPE: PRT; ORGANISM: M.catarrhalis
US-09-540-236-2570
                                                                                                                                                                                                                                           2 GNLFASFIAD 11
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Sequence 74, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering or INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 74.

LENGTH: 595
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Sequence 2570, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                        Sequence 4688, Application US/09328352
Fatent No. 6562958
GENERAL INFORMATION:
APPLICANT GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 36; DB 4; Length 377 77.8%; Pred. No. 1.38+02; Live 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                1 NGNLFASFIADS 12
                                                                                          66 NANLFAS-IADS 76
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US-09-540-236-2570
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                                                                                                                                                             RESULT 13
US-09-328-352-4688
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US-09-198-452A-74
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LENGTH: 377
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Sequence 210244, Sequence 209563,

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100.0%; Score 60; DB 14; Length 12; 100.0%; Pred. No. 0.00018; ive 0; Mismatches 0; Indels
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Sequence 35, Application US/10092750

Sequence 35, Application US/10092750

Publication No. US20030032157A1

GENERAL IMPORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Wright, Martin C.
TITLE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT PELLOR DATE: 2002-03.07

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR PILLING DATE: 2001-03.07

NUMBER OF SEQ ID NOS: 253

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 12
7 US-10-739-930-8886

5 US-10-424-599-210244

6 US-10-408-765A-2344

6 US-10-408-765A-2344

6 US-10-437-963-135735

6 US-10-632-585-7313

7 US-10-632-585-7313

8 US-10-625-122A-70412

8 US-10-424-599-169281

6 US-10-437-963-1932

7 US-10-437-963-1932

8 US-10-437-963-1932

9 US-10-437-963-1932

9 US-10-425-115-367795

9 US-10-102-806-751

9 US-10-425-115-291781

9 US-10-425-115-291781

1 US-10-425-114-47512

9 US-10-425-114-41019

9 US-10-425-114-65399
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       Conservative
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; ORGANISM: Homo sapiens
US-10-092-750-35
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Matches 12; Conserv
       RESULT 2
US-10-106-698-5361
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Sequence 5361, Ap
Sequence 18, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3277,
Sequence 3272,
Sequence 52549, A
Sequence 52549, A
Sequence 52849, A
Sequence 52849, A
Sequence 52849, A
                                                                                                                                                   November 10, 2004, 16:36:12; Search time 12.8912 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/PcT_Rew PUB.Pepp:*

2: /cgn2_6/ptodata/1/pubpaa/PcT_Rew PUB.Pepp:*

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4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.Pepp:*

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6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBGOMB.Pepp:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBGOMB.Pepp:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBGOMB.Pepp:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBGOMB.Pepp:*

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15: /cgn2_6/ptodata/1/pubpaa/USO9_RW PUB.Pepp:*

16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBGOMB.Pepp:*

16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBGOMB.Pepp:*

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17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBGOMB.Pepp:*

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19: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBGOMB.Pepp:*

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10: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBGOMB.Pepp:*

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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-106-698-5361

4 US-10-106-698-6592

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4 US-10-408-765A-192

6 US-10-408-765A-192

7 US-10-010-0653

7 US-10-425-115-186935

7 US-10-425-115-186935

5 US-10-425-114-5249

5 US-10-425-114-5285

5 US-10-425-114-5285

5 US-10-425-114-43548
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                                                                                                                                                                                                                                                                                                                                                                                                      1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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60
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Match Length
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Perfect score:
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Fublication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tahay, Bing
APPLICANT: Glosh, Badford W.
APPLICANT: Glosh, Badford W.
APPLICANT: Glosh, Gary M.
APPLICANT: Warnock, Dale E.
APPLICANT: Glosh, Gary M.
APPLICANT: Warnock, Dale E.
AITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 192
LENGTH: 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 9; Length 226; Pred. No. 10; Mismatches 1; Indels
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: USA
COUNTY: SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM:
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM:
COMPUTER: DEACHTIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-UN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSSEMMAN Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/POCKET NUMBER: 660088.416
TELECHONE: (200) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELBERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2.26 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
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Best Local Similarity 90.09
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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US-09-098-079-18
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     APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polymuclectides and Polypeptide
FILE REPERENCE: PAGGSP1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT PILING DATE: 2002-03-27
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 1090-09-28
PRIOR FILING DATE: 1990-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6592, Application US/10106698
Sequence 6592, Application US/10106698
Sequence 6592, Application US/10106698
Sequence 6592, Application No. US20030109690A1
GREEAL INFORMATION:
GREEAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-19-29
PRIOR FILING DATE: 1999-19-30
NUMBER: OF SEQ ID NOS: 8564
SOFTWARE: PATCHTIN VET: 3.0
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Patent No. US20020064733A1
GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Gloven, Scumitra S.
APPLICANT: Clevenger, William
APPLICANT: Fahy, Eoin F.
APPLICANT: Davis, Robert E.
ATTLE OF INVENTION: EXTRAMITOCHONDBRIAL DNA
TITLE OF INVENTION: EXTRAMITOCHONDBRIAL DNA
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Pred. No. 2.4;
0; Mismatches
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NGNLFASFIA 10
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; ORGANISM: Homo sapiens
US-10-106-698-5361
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US-10-106-698-6592
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US-10-106-698-6592
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5361
LENGTH: 53
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LENGTH: 58
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US-09-098-079-18
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US-10-425-115-362727
; Sequence 362727, Application US/10425115
; Publication Wo. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; SEQ ID NOS: 369326
; SEQ ID NOS 65227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.3%; Score 38; DB 17; Length 85; 50.0%; Pred. No. 20; ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORCANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_93981C.1.pep
US-10-425-115-362727
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77.8%;
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Best Local Similarity 50.0
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Oryza sativa
FEATURE:
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; Sequence 186935, Application US/10425115
; Sequence 186935, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yibua
; APPLICANT: Zhou, Yibua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 186935
; LENGTH: 79
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                                                                                                                                                                                                     Sequence 2, Application US/10010065
; Publication No. US200201443001
; General No. US200201443001
; GENERAL INFORMATION:
; APPLICANT: Allah, Keith D.
; APPLICANT: Moore, Wailiam
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CLUCAGON
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; FILE REFERENCE: R-648
CURRENT APPLICATION NUMBER: US/10/010,065
; CURRENT APPLICATION NUMBER: US 60/251,804
; PRIOR PILING DATE: 2001-12-06
; PRIOR PILING DATE: 2001-12-06
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LANGTH: 485
; TABGET INPERIOR OF SECTION OF 
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US-10-425-115-186935
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Matches 7; Conservative
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178 HGNLFASFV 186
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ORGANISM: Mus musculus
US-10-010-065-2
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ORGANISM: Zea mays
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Gaps

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Sequence 14140'0, Application US/10437963
; Sequence 14140'0, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Chou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brazauk, Brad
; APPLICANT: Brazauk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 103.21218
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 14470
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Pred. No. 25;
0, Mismatches 2; Indels
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US-10-437-963-141470
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2 NENLFASFI 10

RESULT

RESULT 10 US-10-425-114-52549

Sequence 52549, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:

```
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Screen, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Labaska, Jack E.
APPLICANT: Labaska, Jack E.
APPLICANT: Labaska, Jack E.
APPLICANT: Labaska, Jack E.
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43548
LENGTH: 527
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Foblication No. US20040216190A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 38-21 (53377) B

CURRENT RAPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

LENGTH: 527
                  APPLICANT: Cao, Yongwei Title OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NOS: 73128 LENGTH: 327
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US-10-425-114-52852
                                                                                                                                                                                                                                                                                                                                                                                                   63.3%; Score 38; DB 15; 72.7%; Pred. No. 88; iive 0; Mismatches 3
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ORGANISM: Glycine max
FEATURE:
FATURE:

OTHER INFORMATION: Clone ID: 700726816_FLI.pep
US-10-425-114-43548
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Sequence 43548, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Glycine max
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US-10-739-930-8886
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Publication No. US20040072774A1
GENERAL INFORMATION:
APPLICANT: COLUMBIA UNIVERSITY
APPLICANT: Manfredi, Glovanni
APPLICANT: Schon, Eric
TITLE OF INVENTION: METHODS FOR EXPRESSING AND TARGETING MITOCHONDRIA-DNA-ENCODED
TITLE OF INVENTION: PREPTIDES AND USES THEREOF
FILE REFERENCE: 5199-6
CURRENT APPLICATION NUMBER: US/10/371,592
CURRENT APPLICATION NUMBER: US 60/358,935
PRIOR APPLICATION NUMBER: US 60/358,935
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2.
                                                                  APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwon E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO S2549
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.3%; Score 38; DB 15; Length 222; 72.7%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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US-10-425-114-52549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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US-10-425-114-52852
Sequence 58852, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
```

Query Match 63.3 Best Local Similarity 72.7 Matches 8; Conservative

TYPE: PRT ORGANISM: Glycine max

FEATURE:

US-10-371-592-2

TYPE: PRT) ORGANISM: Homo sapiens US-10-371-592-2

g ð

Query Match Best Local Similarity Matches 8; Conserv

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RESULT 15

US-10-424-599-210244

IS-aquence 210244, Application US/10424599

Sequence 210244, Application No. US20040031072A1

SEQUENCE 210244, Application No. US20040031072A1

SEPPLICANT: La Rosa Thomas J

APPLICANT: Cao Vongweil

APPLICANT: Cao Vongweil

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(3323)B

CURRENT APPLICATION UNMERR: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 285684

SEQ ID NO 210244

LENGTH: 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%; Score 38; DB 15; Length 645; Best Local Similarity 72.7%; Pred. No. 1.8e+02; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure

LOCATION: (1)..(645)

OTHER INFORMATION: unsure at all Xaa locations
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_31879C.1.pep
US-10-424-599-210244
; TYPE: PRT ; ORGANISM: Glycine max ; FEATURE: , OPTER INFORMATION: Clone ID: GLYMA-23APR03-C2174_9.p US-10-739-930-8886
                                                                                                                                                                                                                                                                                        418 NGNLKTSFCAD 428
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Search completed: November 11, 2004, 01:28:17 Job time : 13.9412 secs

536 NGNLKTSFCAD 546

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein November 10, 2004, 12:29:32; Search time 2.67358 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

US-10-092-750-35 60 Perfect score:

1 NGNLFASFIADS 12 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	H+-transporting tw	H+-transporting tw	H+-transporting tw	H+-transporting tw	glucagon receptor	glucagon receptor	H+-transporting tw	H+-transporting tw	H+-transporting tw	H+-transporting tw	cobalamin biosynth	phosphate uptake A	potassium-transpor	potassium-transpor	zinc-finger protei	H+-transporting tw	TcaB protein [impo	probable ThrC2 thr	ribosomal protein	site-specific DNA-	carboxylesterase,	phosphomannomutase	phosphomannomutase	cation efflux syst	H+-transporting tw	H+-transporting tw	hypothetical prote	oxidoreductase ycg
SUMMARIES	ΠD	PWHU6	F59153	T10977	T11498	JC4363	JQ1957	PWMS6	T11145	T11055	804752	D90153	H95946	A11409	AH1785	T18297	T37052	F90035	G95293	S78395	S02856	A75250	A72124	In	C96945	T11433	2518	∞	8665
	Length DB	56	92	56	92	35	92	56	226 2	56	56	93	9	61	61		99	02	84	20	03	40	98	98	99	56	226 2	07	57
æ	Query Match	70.0	0	70.0	ů.	•	66.7	63.3	63.3	m.	m m	e,	63.3	63.3	63.3	63.3	61.7	61.7	61.7	60.09	60.09	60.09	0.09	60.0	60.09	58.3	58.3	58.3	58.3
	Score	42	42	42	40	40	40	38	38	38	38	38	38	38	38	38	37	37	37	36	36	36	36	36	36	35	35	35	35
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RESULT 2

H-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - western lowland gorilla mitor N;Alternate names: hydrogen ion-transporting ATP synthase protein 6 C;Species: mitochondrion Gorilla gorilla (western lowland gorilla) C;Species: mitochondrion Gorilla gorilla (western lowland gorilla) C;Accession: F59153
B;Xu, X.; Arnason, U.
Mol. Biol. Evol. 13, 691-698, 1996
A;Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla. A;Reference number: 217269; MUID:96212991; PMID:8676744
A;Accession: F59153
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown; translatect A;Residues: 1-226 < xUX>
A;Residues: 1-226 < xUX>
A;Residues: L226 < xUX>
A;Residues: L226 < xUX>
A;Residues: bold and a complete sequence not shown; translation not shown; translation is not annotated in GenBank entry GGMITG, release 114.0

hypothetical prote

H72683

0 394

58.3

32

59

probable transposa	hypothetical prote	F25A4.24 [imported	beta-fructofuranos	photomorphogenesis	semaphorin I precu	hypothetical prote	hypothetical prote	H+-transporting tw	Htransporting tw						
T36649	F82354	C96777	T12083	T06560	A49423	828700	B65045	PWBO6	T11446	T11407	S41840	826156	T11368	T11862	T11252
7	0	N	~	N	(7)	N	N	Н	~	0	~	~	0	~	N
407	436	642	651	672	711	137	210	226	226	226	226	226	226	226	226
58.3	58.3	58,3	58.3	58.3	58.3	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7	56.7
35	35	35	35	32	35	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Nature 290, 457-465, 1981

A,Title: Sequence and organization of the human mitochondrial genome.

A,Reference number: A00151; MUID:81173052; PMID:7219534

A,Accession: A01043

A,Accession: A01045

A,Molecule type: DNA

A,Residues: 1-226 <AND>
A,Genetics: WNIPROT:P00846; GB:J01415; GB:M12548; GB:M58503; GB:M63932; GB:M63931; C,Genetics: M,Genetics: GB:SITATPP
A,Gene: GDB:MATPP
A,Gene: GDB:MATPP
A,Gene: GDB:MATPP
A,Genetic code: GGCI
A,Represence GGCI
A,Represence GGCI
A,Genome: mitochondrion
A,Genome: mitochondrion; Mitochondrion; Oxic
                                                          H-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - human mitochondrion N,Alternate names: hydrogen ion-transporting ATP synthase protein 6 (5)pecies: mitochondrion Homo sapiens (man) (5)pecies: mitochondrion Homo sapiens (man) (5)pecies: 22-May-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004 (5)Accession: A01049 (8)Accession: A01049 (8) Parrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin, c.
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RESULT 1
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us-10-092-750-35.rpr

C;Genetics:

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A;Title: The complete nucleotide sequence of the domestic dog (Canis familiaris) mitochor A;Reference number: 217276; MUID:99097286; PMID:9878232
A;Accession: Til498
A;Accession: Til498
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI A;Molecule type: DNA
A;Residues: 1-226 <KIM>A;Accessives: 1-226 <KIM>A;Cross-references: UNIPROT:092Z62; EMBL:U96639; NID:94154170; FID:94154176; PIDN:AAD0476; G;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Genome: mitochondrion
A Genetic ode: 8GC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: Q61606; GB: L38612; NID: 97274387; PIDN: AAF44749.1; PID: 9727438 C. Comment: This receptor is a plasma membrane glycoprotein that belongs to a subfamily of genolysis and gluconeogenesis in li ver and insulin secretion by beta cells. C; Genetics:
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C, Superfamily: glucagon receptor
C, Superfamily: glucagon receptor
F, Reywords: glycoprotein; receptor
F, 1-27/Domain: signal sequence #status predicted <SIG>F, 28-485/Product: glucagon receptor #status predicted <MID>F, 145-168/Domain: transmembrane #status predicted <TMI>F, 145-168/Domain: transmembrane #status predicted <TMI>F, 147-28/Domain: transmembrane #status predicted <TMI>F, 28-48-28/Domain: transmembrane #status predicted <TMI>F, 26-28/Domain: transmembrane #status predicted <TM5>F, 36-36/Domain: transmembrane #status predicted <TM6>F, 31/Domain: transmembrane #status predicted <TM6>F, 31/Domain: transmembrane #status predicted <TM6>F, 31-40-28/Domain: transmembrane #status predicted <TM6>F, 31-40-28/Domain: transmembrane #status predicted <TM6>F, 31-40-28/Domain: transmembrane #status predicted <TM6>F, 31-40-40-5/Domain: transmembrane #status predicted <TM6>F, 31-40-40-5/Domain: transmembrane #status predicted <TM6>F, 31-40-5/F, 31-40-40-5/F, 3
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N;Alternate names: GLP-1 receptor homolog, hepatic
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1957; A46211; S29689
R;Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Cauvin, A.; Stievenart, M.; Charistophe,
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R;Burcelin, X., Li, J.; Charron, M.J.
Gene 164, 305-310, 1995
A;Title: Cloning and sequence analysis of the murine glucagon receptor-encoding gene.
A;Reference number: JC4363; MUID:96069600; PMID:7590348
A;Accession: JC4363.
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Pred. No. 11;
2; Mismatches
Phylogenet. Evol. 10, 210-220, 1998
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77.88;
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178 HGNLFASFV 186
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Best Local Similarity
Matches 9; Conserv
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Matches 7; Conserv
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A; Residues: 1-485 <BUR>
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                                                                                       A.Genome: mitochondrion
A.Genetic code: SGC1
C.Superfamily: H+-transporting ATP synthase protein 6
C.Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Residues: 1-226 <LIN>
;Cross-references: UNIPROT:Q35915; EMBL:AF034253; NID:g4958951; PID:g4958957; PIDN:AAD3
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A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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Natanabe, T.; Hayashi, Y.; Kimura, J.; Yasuda, Y.; Saitou, N.; Tomita, T.; Ogasawara, Jochem. Genet. 24, 385-396, 1986.

Title: Pig mitochondrial DNA: polymorphism, restriction map orientation, and sequence in the second map or second sequence is the second map or second second map or second sequence is the second map or second second map or second second second map or second seco
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submitted to the EMBL Data Library, February 1999
A.Description: The complete mitochondrial DNA sequence of the pig (Sus scrofa).
A.Reference number: Z17370
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                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 42; DB 2; Length 226;
larity 90.0%; Pred. No. 2;
Conservative 0; Mismatches 1; Indels
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Molecule type: DNA;
Residues: 1-226 <URS>
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Residues: 1-28;219-226 <WAT>
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Best Local Similarity
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Best Local Similarity
'Loc 9; Conserv?
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                                                            A; Gene: ATPase6
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C;Genetics:

T11498

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H-transporting two-sector ATPase (BC 3.6.3.14) protein 6 - fruit bat (Artibeus jamaicens C,Species: mitochondrion Artibeus jamaicensis C,Species: mitochondrion Artibeus jamaicensis C,Species: mitochondrion Artibeus jamaicensis C,Species: mitochondrion Artibeus jamaicensis C,Accession: T11145
R,Pumo, D.E.; Finamore, P.S.; Franek, W.R.; Phillips, C.J.; Tarzami, S.; Balzarano, D. J. Mol. Evol. 47, 709-771, 1998
A,Fittle: Complete mitochondrial genome of a neotropical fruit bat, Artibeus jamaicensis, A,Accession: T11145
A,Accession: T1145
A,Accession: T1146
A,Molecule type: DNA
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Gorsa-references: UNIPROT:099599; EMBL:AF061340; NID:g4164474; PID:g4164480; PIDN:AADDGECGENERICS:
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C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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804752
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - rat mitochondrion
C;Species: mitochondrion Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990
C;D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 226;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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A,Accession: A46211
A,Accession: A46211
A,Accession: A46211
A,Rebifusing Fellminary; nucleic acid sequence not shown; not compared with conceptual trafableoule type: mRNA
A,Residues: 1-37, 'W', 38-215, 'W', 217-323, 'V', 325-485 <JEL>
A,Roperimental source: liver
A,Note: sequence extracted from NCBI backbone (NCBIP:127785)
C,Genetics: 132/3, 168/2; 220/3; 407/3
A,Introns: 132/3, 168/2; 220/3; 407/3
C,Superfamily: glucagon receptor; glycoprotein; liver; phosphoprotein; transmembrane #status predicted <TML>
F,144-167/Domain: transmembrane #status predicted <TML>
F,151-194/Domain: transmembrane #status predicted <TMS>
F,227-251/Domain: transmembrane #status predicted <TMS>
F,305-324/Domain: transmembrane #status predicted <TMS-
F,3
                                               Aritle: Small introns in a hepatic cond. Askeference number: J01957; MUD:93213282; PMID:8384842
A,Reference number: J01957; MUD:93213282; PMID:8384842
A,Accession: J01957
A,Accession: J01957
A,Accession: J01957
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A,Accession: J01957
A,Residues: 1-485 <SVO
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A;Genterio code: 8GC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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Pred. No. 11;
2; Mismatches 0; Indels
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88.9%; Pred. No. 11;
tive 0; Mismatches 1; Indels
Biochem. Biophys. Res. Commun. 191, 479-486, 1993
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77.8%;
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Best Local Similarity 77.8
Matches 7: Conservative
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Matches 8, Conservative
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative

A; Genome: mitochondrion

C;Genetics:

A;Residues: 1-226 <GAD>

2 NENLFASFI 10

1 NGNLFASFI 9

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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
CiAccession: Al1409
CiAccession: Al1409
Cipate: 2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Coipate: 2004 Marst, U.
Cipate: 2004 Marst, U.
Cipate: 2004 Marst, U.
Cipate: 2004 Marst, U.
Cipate: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: Al1400.
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Modecule type: DNA
A,Residues: 1-561 <GLA>
A,Cross_references: UNIPROT:Q8Y326, GB:NC_003210, PIDN:CAD00895.1, PID:g16412182, GSPDB:C
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A;Molecule type: DNA
A;Residues: 1-561 GCLA-
A;Cross-references: UNIPROT:Q927F9; GB:AL592022; PIDN:CAC98056.1; PID:g16415365; GSPDB:GR
A;Experimental source: strain Clip11262
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R;Glaser; P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Doninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Auchors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Title: 'Comparative genomics of Listeria species.
A;Title: 'Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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                                                                                      63.3%; Score 38; DB 2; Length 505; 88.9%; Pred. No. 27; tive 0; Mismatches 1; Indels
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C; Genetics:
A; Gene: KdpA
C; Superfamily: H+/K+-exchanging ATPase subunit A
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NGSAFAGFAADT 479
                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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A; Gene: phoT; SMb21174
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                                      A; Genome: plasmid
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                                   A, Cross-references: UNIPROT: P05504; EMBL: X14848; NID: 9854269; PIDN: CAA32959.1; PID: 91346
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phosphate uptake ABC transporter permease protein phor [imported] - Sinorhizobium melilot C; Species: Sinorhizobium meliloti C; Species: Sinorhizobium meliloti C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Accession: H59546 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernath Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 #Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Nolecule type: DNA
A;Rosidues: 1-505 cKUR>
A;Cross-references: UNIPROT:Q52909; GB:AL591985; PIDN:CAC49240.1; PID:g15140726; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Apman, R.W.; Jones, T.
Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Science 259, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Reference number: Aş6039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Modecule type: DNA
A;Residues: 1-293 «KRR»
A;Cross-references: UNIPROT:Q980Y9; GB:AE006641; NID:g13813263; PIDN:AAK40483.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
                                                                                                                                                              63.3%; Score 38; DB 2; Length 226; 88.9%; Pred. No. 11; ative 0; Mismatches 1; Indels
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C; Superfamily: Cobalamin biosynthesis protein CbiG

A;Accession: D90153

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Query Match

A; Gene: cbiG

C;Genetics:

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C; Genetics:

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1 NGNLFASFIADS 12
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incipar protein FOG-2 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Jo-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18297
R;Tevosian, S:G: Deconinck, A.E.; Cantor, A.B.; Rieff, H.I.; Fujiwara, Y.; Corfas, G:; Proc. Natl. Acad. Sci. US:A. 96; 950-955, 1999
A;Title: FOG-2: A novel GATA-family cofactor. related to multitype zinc-finger proteins FA;Reference number: Z18866; MUD:99128343; PMID:9927674
A;Accession: T18297
A;Accession: T18297
A;Accession: T18297
A;Accession: T18297
A;Cosper-references: UNIPROT:Q8CCH7; EMBL:AF107306; NID:g4206772; PID:g4206773; PIDN:AAD1A;Gene: Fog-2 Query Match 63.3%; Score 38; DB 2; Length 1151; Best Local Similarity 70.0%; Pred. No. 63; Matches 7; Conservative 2; Mismatches 1; Indels

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RX MEDINIBE-22560454; PubMed=12620789;

RX MEDINIBE-22560454; PubMed=12620789;

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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 26, Last an
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Pred. No. 20;
2; Mismatches 1; Indels
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PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
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ATP synthase a chain (EC 3.6.3.14) (ATPase protein Name=MTATP6; Synonyms=ATP6; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heteroplasmy.";
Am. J. Hum. Genet. 46:428-433(1990)
                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=95132634; PubMed=7530363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92098084; PubMed=1757091;
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VARIANT NARP ARG-156.
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=9606;
                                              Mitochondrion.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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TISSUB=perigheral blood;
TISSUB=perigheral blood;
MEDILINE=98403943; PubMed=9734874;
Tartaglia M., Saulle E.;
"Rapid communication: nucleotide sequence of porcine and ovine tRNA(kys) and ATPase8 mitochondrial genes.";
J. Anim. Soi. 76:2207-2208 (1998).
EMBL; AF039170; AAD05065.1;
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                                                                                                                                          SEQUENCE FROM N.A.
TISSUB=Peripheral blood;
MEDLINE=98403943; PubMed=9734874;
Tartaglia M., Saulle E.;
"Rapid communication: nucleotide sequence of porcine and ovine tRNA(Lys) and AFPase8 mitochondrial genes.";
J. Anim. Sci. 76:2207-2208(1998).
EMBL; AF039170; AAD506561;
GO; GO:0005739; C:mitochondrion; IEA.
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Pred. No. 1.4;
0; Mismatches 1; Indels
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Pred. No. 1.4;
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SEQÜENCE 22 AA; 2411 MW; D440C56CAE0EAIC9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATPase subunit 6 (Fragment)
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02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last seq
02-WAR-2004 (TrEMBLrel. 27, Last ann
ATPase subunit 6 (Fragment).
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Best Local Similarity
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                                                              Sus scrofa (Pig).
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ATP6_HUMAN
ID ATP6_HC
AC P00846;
DT 21-JUL
DT 21-JUL
DT 05-JUL
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RESULT 3
AAD05065
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AAD0
DT 02-M
DT 02-M
DE ATP6
OC MANT
OC MANT
OC MANT
OC MANT
CO MANT

Matches

Matches

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Horai S., Hayasaka K., Kondo R., Tsugane K., Takahata N., "Recent African origin of modern humans revealed by complete sequences of hominoid mitochondrial DNAs."; Proc. Natl. Acad. Sci. U.S.A. 92:532-536 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT TYR-90.

MEDLINE=22062553; PubMed=12022039;
Silva W.A. Ur., Bonatto S.L., Holanda A.J., Ribeiro-Dos-Santos A.K.,
Salvao B.M., Goldman G.H., Abe-Sandes K., Redriguez-Delfin L.,
Barbosa M., Paco-Larson M.L., Petzl-Erler M.L., Valente V.,
Santos S.E., Zago M.A.;
Mitochondrial genome diversity of native Americans supports a single early entry of founder populations into American.";
Am. J. Hum. Genet. 71:187-192(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marzuki S., Noer A.S., Lertrit P., Thyagarajan D., Kapsa R., Utthanaphol P., Byrne E., "Normal variants of human mitochondrial DNA and translation products: the building of a reference data base.";
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MEDDINE-89072713; PubMed=3201231;
Wallace D.C., Singh G., Lott M.T., Hodge J.A., Schurr T.G.,
Lezza A.W., Elsas L.J. II, Nikoskelainen E.K.;
"Mitochondrial DNA mutation associated with Leber's hereditary optic
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Lamminen T., Majander A., Juvonen V., Wikstroem M., Aula P.,
Nikoskelainen E., Savontaus M.-L.;
"A mitochondrial mutation at nt 9101 in the ATP synthase 6 gene
associated with deficient oxidative phosphorylation in a family with
Leber hereditary optic neuroretinopathy.";
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILES-81173022; PubMed=7219534;
MEDILES-81173022; PubMed=7219534;
Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.;
"Sequence and organization of the human mitochondrial genome.";
Nature 290:457-465(1981).
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MEDILMES9331018; PubMed=8395787;
de Vries D.D., van Engelen B.G.M., Gabreels F.J.M., Ruitenbeek
van Oost B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A second missense mutation in the mitochondrial ATPase 6 gene Leigh's syndrome.";
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Holt I.J., Harding A.E., Petty R.K., Morgan-Hughes J.A.;
"A new mitochondrial disease associated with mitochondrial DNA
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EMBL; D38112; BAA07295.1; -.
EMBL; AF465962; AAN14772.1; -.
PIR; A01049; PWHU6.
Genew; ANGNC:7414; MTATP6.
Reactome; P00846; -.

EMBL; J01415; AAB58948.1; -. EMBL; V00662; CAA24031.1; -.

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Am. J. Hum. Genet. 56:1238-1240(1995).

[9]
VARIANT FESN PRO-217.
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422; PubMed=7668837;
MEDLINE=95398422. PubMed=7668837;
MARGARATAIN D., Shanske S., Vazquez-Memije M., de Vivo D., Dimauro S.;
"A novel mitochondrial ATPase 6 point mutation in familial bilateral striatal necrosis.";
                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the ATPase A chain family.
                                           PRO-217
                                                                                                                                                             VARIANT THR-155.
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VARIANT LS PRO-217.
WEDLINES=98161883; PubMed=9501263;
MEDLINES=98161883; PubMed=9501263;
Dionisi-Vici C., Seneca S., Zeviani M., Fariello G., Rimoldi M.,
Bertini E., De Meirleir L.;
Fulminant Leigh syndrome and sudden unexpected death in a family with
the T9176C mutation of the mitochondrial ATPase 6 gene.";
J. Inherit. Metab. Dis. 21:2-8(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98127994; PubMed=9461455; Rieder M.O., Taylor S.L., Tobe V.O., Nickerson D.A.; Raleder M.O., Taylor S.L., Tobe V.O., Nariations using quality-based "Automating the identification of DNA variations using quality-based fluorescence re-sequencing: analysis of the human mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT LS ARG-156.
MEDLINE=98220421; PubMed=9556461;
Takahashi S., Makita Y., Oki J., Miyamoto A., Yanagawa J., Naito E., Goto Y., Okuno A.;
"De novo mtDNA nt 8993 (T-G) mutation resulting in Leigh syndrome.";
Am. J. Hum. Genet. 62:717-719(1998).
                                                                                                          MEDLINE=97416654; PubMed=9270604; Campos Y., Martin M.A., Rubio J.C., Solana L.G., Garcia-Benayas C. Campos Y., Martin M.A., Rubio J.C., Solana L.G., Garcia-Benayas C. Terradas J.L., Arenas J.; Leigh syndrome associated with the T9176C mutation in the AFPase gene of mitochondrial DNA."; Meurology 49:595-597(1997).
Neurol. 38:468-472(1995).
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Mucleic Acids Res. 26:967-973(1998).

Nucleic Acids Res. 26:967-973(1998).

-! FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.
-!- CATALYTIC ACTIVITY: ATP + H(2) O + H(+)(In) = ADP + phosphate + H(+)(Out).
-!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

DIESTARY MEMORIAGE.

Weakness, ataxia, and retinitis pigmentosa (NARP) [WIM:551500].

DISEASE: Defects in MTATP6 are a cause of Leber's hereditary optic
DISEASE: Defects in MTATP6 are a cause of Leber's hereditary optic
DISEASE: Defects in MTATP6 are a cause of Leber's hereditary optic
atrophy. LHON is a maternally inherited disease resulting in acute
bliateral blindness due to retinal degeneration predominantly in
young man. Cardiac conduction defects and neurological defects
have also been described.

DISEASE: Defects in MTATP6 are a cause of Leigh syndrome (LS)
MIM:256000]. LS is a severe neurological disorder characterized
by bilaterally symmetrical necrotic lesions in subcortical brain

DISEASE: Defects in WTATP6 may be a cause of familial bilateral striatal necrosis (FBSN). FBSN is a neurological disorder resembling Leigh syndrome.

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CP(0); Disease mutation; Hydrogen ion transport;
Leber hereditary optic neuropathy; Leigh syndrome; Mitochondrion;
Polymorphism; Transmare.
VARIANT
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PRINTS: PROULTS; ATP-SYNTE, A: 1.

TIGREAMS; TIGROITS! ATP-SYNTE, Cor. A: 1.
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035915; 079878; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6). Name-MTATP6; Synonyms-ATP6, ATPASE6; Sus scroid (Pig). 226 AA STANDARD; RESULT S ATP6 PIG ID ATP6 PIG OCCOSSION

Mitochondrion. Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus. NCBI_TaxID=9823,

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-1- RUBONIT: F-type ArPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- STHILARITY: Belongs to the ArPase A chain family.
EMBL, AYS19486; AAR91237.1; -
CO, GO:0005739; C:mitochondrion, IEA.
InterPro; IPR000568; ATPSYNL Asub.
PRIMTS, PR00112; ATPASEA.
TIGRRAMS; TIGR01131; ATP SYNL 46 or A; 1.
PROSITE; PS00449; ATPASEA.
TIGRRAMS; TIGR01131; ATP SYNL 6 or A; 1.
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Irwin J.A., Parsons T.J.;

Isingle nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-0(2004).

-! FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane (By similarity).

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                             SEQUENCE FROM N.A. Statistics, Sukernik R.I., Derbeneva O.A., Volodko N.V., Statistovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V., Torroni A., Ruiz-Pesini E., Brown M.D., Lott M.T., Hosseini S.H., Huoponen K., Wallace D.C., "Mitochondrial DNA Diversity in Indigenous Populations of Southern "Mitochondrial DNA Diversity in Indigenous Populations of Southern Extent of Siberia, and the Origins of Native American Haplogroups."; Ann. Hum. Genet. 0:0-0(2004).
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                                                                                                                                                                                                                                                                                                              Ann. Hum. Genet. 0:0-0(2004).

-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane (By similarity).

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
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SEQUENCE 226 AA; 24783 MW; 61D5F6712A993712 CRC64;
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Last annotation update)
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               Homo sapiens (Human).
Mitochondrion.
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Mitochondrion.
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SEQUENCE FROM N.A.
PubMed=14760490;
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Name=ATP6;
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                                                                                                                                                        SECUENCE FROM N.A.
STRAIN=Landrace; TISSUE=Heart;
STRAIN=293653306; Pubmed=10433971;
MADILINE=993653306; Pubmed=10433971;
Lin C.S., Sun Y.L., Liu C.Y., Yang P.C., Chang L.C., Cheng I.C.,
Mao S.J.T., Huang M.C.;
"Complete nucleotide sequence of pig (Sus scrofa) mitochondrial genome and dating evolutionary divergence within artiodactyla.";
Gene 236:107-114(1999).
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"Pig mitochondrial DNA: polymorphism, restriction map orientation, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H(+)(Out).
-!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE OF 1-37 FROM N.A.
MEDLINE=86295557; PubMed=3017295;
Watanabe T., Hayashi Y., Kimura J., Yasuda Y., Saitou N., Tomita T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence data.";
Biochem. Genet. 24:385-396(1986).
-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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                                                                Ursing B.M., Arnason U.; "The complete mitochondrial DNA sequence of the pig (Sus scrofa)."; J. Mol. Evol. 47:302-306(1998).
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PRINTS; PR00123; ATPASEA.
TIGRRAMS; TIGR01131; ATP synt 6 or A; 1.
PROSITE; PS00449; ATPASEA; 1.
PROSITE; PS00449; ATPASEA; 1.
CRON, Hydrogen ion transport; Mitochondrion; Transmembrane.
CONFLICT 30 37 LPPTPKRL -> SLYLHDNT (in Ref. 3).
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                  SEQUENCE FROM N.A.
MEDLINE=98404150; PubMed=9732457;
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Matches 9; Conservative
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O5-JUL-2004 (
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core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), peta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the ATPase A chain family.

R MRBL, AY495323; AR595301. -.

R GO; GO:0005739; C:mitcchondrion; IEA.

InterPro; IPR000568; ATPSYNL Asub.

R FRIMTS; PR00123; ATP-SYNL Asub.

R FRIMTS; PR00123; ATP-SYNL A: 1.

R PRIMTS; PR00129; ATPASE A; UNKNOWN 1.

R PRIMTS; PR00449; ATPASE A; UNKNOWN 1.

R PRIMTS; PR0449; ATPASE A; UNKNOWN 1.

R PRIMTS; PR05456 A; 24783 MW; 578BEB0432E140FA CRC64;
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Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forenaic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
Int. J. Legal Med. 0:0-0(2004).
-: FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane
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-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Transmembrane; Transport.
SEQUENCE 226 AA; 24797 WW; 578FFF1436F550FA CRC64;
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PROSITE; PS00449; ATPASE_A; 1.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
ATP synthase F0 subunit 6.
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Best Local Similarity 90.0
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-! CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate + H(+)(Out).

-!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunite: alpha (3), peran (1), delta(1), epsilon(1).

-!- SUBCELUCIAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the ATPase A chain family.

EMBL; AY495295; AAR95166.1; -..

EMBL; AY495295; ARR95166.1; -..
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Coble M.D. Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.; 
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 226 AA; 24775 MW; B5BCIEE8DBF54F0E CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 6.
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Last sequence update)
Last annotation update)
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TIGRPAMS, TIGR01131, ATP_SYNt_6_or_Ā; 1.
PROSITE; PS00449, ATPASE_Ā; 1.
                                                                                                                                                                                                                                                                                     PRT;
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Best Local Similarity 90.v
Best Aca 9; Conservative
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2 NENLFASFIA 11
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Fri Nov 12 14:55:18 2004

SEQUENCE FROM N. PubMed=14760490;

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                                              Coble M.D., Just R.S., O'Callaghan J.B., Letwanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.,
Irwin J.A., Parsons T.J.,
"Single modleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane (By similarity).
-!- CARTANTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + phosphate +
                                                                                                                                                                                                                                         -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), denma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).
-! SUBELLIULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the ATPase A chain family.
BMBL, AX455288; AAR95075.1; --
GO, GO:005739; C:mitcochondrion; IEA.
InterPro: IPR00168; ATPSYAL Asub.
PETM: PR00119; ATPSYALE A: 1.
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Irwin J.A., Parsons T.J.,
"Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-i- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane
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-!- SUBUNIT: F-type ArPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1).

-!- SUBCELEULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to ArPase A chain family.
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CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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TIGRRAMs; TIGR01131; ATP synt_6 or_A; 1.
PROSITE; PS06449; ATPASE_A; 1.
CF(0); Hydrogen ion transport; Mitochondrion;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 42; DB 2; Length 226; 90.0%; Pred. No. 14; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 AA; 24817 MW; 68BOFF0F37455207 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 6.
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Best Local Similarity 90.0.
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RESULT 13

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-1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunites alpha(3), bened(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunites: a, b, and c (By similarity).
-1- SUBCELULIAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to the ATPase A chain family.

EMBL, AY458229; AR493308.1; -
EMBL, AY458239; C:mitochondrion; IEA.

InterPro; IPR000568; ATPSYMIT, ASub.

PFO0119; ATP-SYMIT, A: 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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GO, GO:0005739; C:mitochondrion; IEA.
InterPro; IFR000568; ATPSynt Asub.
Pfam; PF00119; ATP-synt A: 1.
PRINTS; PR00123; ATPASEA.
TIGRRAMS; TIGRO1131; ATP Synt 6 or A; 1.
PROSTIE; PS00449; ATPASEA; UNKNOWN 1.
CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
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                                                                                                                                           / Match 70.0%; Score 42; DB 2; Length 226; Local Similarity 90.0%; Pred. No. 14; 19 Conservative 0; Mismatches 1; Indels
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                                                                                                   Transmembrane; Transport.
SEQUENCE 226 AA; 24787 MW; 68B6236430292207 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP synthase F0 subunit 6.
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TIGRFAMS; TIGR01131; ATP Synt 6 or A; 1.
PROSITE; PS00449; ATPASE A; 1.
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Guery Match
Best Local Similarity 90.00,
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SEQUENCE 226 AA; 2478
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                                                                                                                                                Query Match
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Matches
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70.0%;
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Best Local Similarity 90.v.,
Best Local Similarity 90.v.,
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Q6RQ23
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C. Int. J. Legal Med. 0:0-0.02004).

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Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 14;
0; Mismatches 1; Indels
                                                                                                                 Created)
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                                          226 AA
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TIGRFAMS, TIGR01131, ATP_SYNt_6 or_A, 1.
PROSITE, PS00449, ATPASE A, 1.
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                                          PRT;
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05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
ATP synthase F0 subunit 6.
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Best Local Similarity 90..
Conservative
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                                                                                                                 05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                       ATP synthase F0 subunit
Name=ATP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NGNLFASFIA 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ATP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
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                                     Q6RNI4
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OGERPH
AC GERPH
AC GERPH
DT 05-JU
DT 0

      90 RAD

      90 RAD
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C. -: CALCALLY

C. -: SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five core - and CF(0) - the membrane proton channel. CF(1) has five care - and CF(0) - the membrane proton channel. CF(1) has five care alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)

C. -: SUBCRIUGAR LOCATION: Integral membrane protein (By similarity).

C. -: SIMPLIANITY: Belongs to the ATPase A chain family.

REMBL, AX495199, AAR9348.1; -.

DR GO; GO; GOS739; C: mitochondrion; IEA.

BR PÉAN; PF00119; ATP-Synt Asub.

DR PÉAN; PF00113; ATP-Synt Asub.

DR PRONIE; PR00123; ATPASEA.

DR PRONIE; PR00449; ATPASEA.

DR PROSTE; PS00449; ATPASE A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H(+) (Out).

-!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(1), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the ATPase A chain family.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-!- FUNCTION: Key component of the proton channel; it may play a
direct role in the translocation of protons across the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
                                                                                                                              (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
Transmembrane; Transport
SEQUENCE 226 AA; 24773 MW; 68B0ECAC0D655207 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incerpro; IPR000568; ATPSYNL Asub.
Pfam: PF00119; ATP-SYNL A: 1.
PRINTS: PR00123; ATPASEA.
TICRPAMS; TICR0111; ATP SYNL 6 or A: 1.
PROSITE; PS00449; ATPASE A: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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CF(0); Hydrogen ion transport; Ion transport; Mitochondrion; Transmembrane; Transport. SEQUENCE 226 AA; 24773 MW; 73B0FF12EDF79903 CRC64; S K K

0; Gaps Query Match 70.0%; Score 42; DB 2; Length 226; Best Local Similarity 90.0%; Pred. No. 14; Matches 9; Conservative 0; Mismatches 1; Indels

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1 NGNLFASFIA 10 | | | | | | | | | | 2 NENLFASFIA 11

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Search completed: November 10, 2004, 13:38:35 Job time: 15.6528 secs

us-10-092-750-36.rai

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VS-091-25-991A-18304

i Sequence 18304, Application US/09252991A

j Sequence 18304, Application US/09252991A

j Sequence 18304, Application US/09252991A

j Patent No. 6551795

j TITLE NO. 6551795

j TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

j TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

j TILE REFERENCE: 107196.136

j CURRENT APPLICATION UNMBER: US 60/074,788

j PRIOR APPLICATION UNMBER: US 60/074,788

j PRIOR PILING DATE: 1998-02-18

j PRIOR PILING DATE: 1998-02-18

j PRIOR FILING DATE: 1998-07-27

j NUMBER OF SEQ ID NOS: 33142

j SEQ ID NO 18304

j LYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21163
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Matches 9; Conser
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, App]
Sequence 31583, A
                                                                                                                     November 10, 2004, 12:32:37; Search time 10.0173 Seconds (without alignments)
191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-18104
US-09-252-991A-21163
US-08-856-4444-2
US-08-856-4444-2
US-08-856-4444-2
US-09-88-1710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-881-710-13
US-09-113-999-2
US-09-113-999-2
US-09-113-999-2
US-09-113-999-2
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US-09-28-91A-21765
US-09-28-91A-21765
US-09-28-91A-21765
US-09-28-91A-21765
US-09-28-91A-311A-4
US-09-38-079-33
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US-09-252-991A-31583
                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                               US-10-092-750-36
155
1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP
                                                                                                                                                                                                                                                                                                                             478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                        OM protein
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Maximum DB
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Gaps

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4; Length 196;

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US-09-252-991A-21163

1 Sequence 21163, Application US/09252991A

2 Sequence 21163, Application US/09252991A

3 Fatent No. 6551795

3 Fatent No. 6551795

4 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

5 TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

5 FILE REFERENCE: 107196.136

6 CURRENT FILING DATE: 1999-02-18

7 PRIOR FILING DATE: 1998-02-18

7 PRIOR FILING DATE: 1998-02-18

7 PRIOR FILING DATE: 1998-07-27

8 PRIOR FILING DATE: 1998-07-27

9 PRIOR FILING DATE: 1998-07-27
27216, A
23740, A
5822, Ap
46698, A
370, App
26815, A
23, Appl
19574, A
24198, A
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51, Appl
5, Appli
7, Appli
                                                                               Sequence
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Sequence
Sequence
                               Sequence
                                                           Sequence
US-09-252-991A-27216
US-09-252-991A-23740
US-09-107-532A-58740
US-09-107-57-46698
US-09-108-452A-370
US-09-108-452A-370
US-09-252-991A-25815
US-09-252-991A-19574
US-09-252-991A-19574
US-09-252-991A-19574
US-09-252-991A-3028
US-09-257-581-5
US-09-602-787A-296
US-09-257-581-5
US-09-257-581-7
US-09-257-981-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-554-612C-1
Sequence 1, Application US/08554612C
Patent No. 5747660
- GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: El PEM PC COMPATIBLE
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: NO. 5747660ember 6, 1995
CLASSIFICATION NUMBER: US/08/554,612C
ATTORNEY/AGENT INFORMATION:
NAME: SAFETWOOM, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
31.3%; Score 48.5; D:
Best Local Similarity 52.6%; Pred. No. 36;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 LLTAPWSTRQG---RLQQA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILTSPWTTSSGLWPRLQKA 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRRACTERISTICS:
LENGTH: 343 amino acids
                                                                                                                                           : 343 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PUBLICATION INFORMATION:
US~08-856-444-2
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-554-612C-1
                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
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                                                                                                                                                                                                      STRANDEDNESS:
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US-09-252-991A-20842
Squence 20842, Application US/09252991A
Squence 20842, Application:
Squence 20842, Application Squence all TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
SPICA PAPLICATION NUMBER: US 60/074,788
SPICA PAPLICATION NUMBER: US 60/074,788
SPICA RAPLICATION NUMBER: US 60/094,190
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                                                                                                                                                   Gaps
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; Sequence 2, Application US/08856444
; Patent No. 5959081
; Patent No. 5959081
; GENERAL INFORMATION:
; APPLICANT: Lecka-Czernik, Beata
; TITLE OF INVENTION: No. 5959081e1 Zinc Binding LIM Protein S2-6
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 149;
                                                                                     Score 49; DB 4; Length 462;
Pred. No. 44;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GLWPRLQKAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D. STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,444
FILING DATE: May 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.3%; Score 48.5; Dl
Best Local Similarity 28.6%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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24 ISSPWATSAAGWP 36
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DESPERS, Phillipe
APPLICANT: DEUBLA, Vincent
APPLICANT: CATTEAU, Adeline
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINS
FILE REFERENCE: 209671US0
CURRENT APPLICATION NUMBER: US/09/881,710
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DESPRES, Phillipe
APPLICANT: DESPRES, Vancent
APPLICANT: DEUBL, Vincent
APPLICANT: CATTEAU, Adeline
TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINE
FILE REPRENCE: 208671US0
CURRENT APPLICATION NUMBER: US/09/881,710
CURRENT APPLICATION NUMBER: 60/212,129
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE PATENTION OF 300
SOFTWARE PATENTED APPLICATION OF 300
LENGTH: 39
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Pred. No. 4.6;
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43.8%; Pred. No. 4.6;
tive 3; Mismatches
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; Sequence 28, Application US/09881710
; Patent No. 6673895
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Dengue virus
US-09-881-710-12
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                                                                                                                                       Sequence 5129, Application US/09583110

Factor No. 6699703

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
CURRENT PRILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: US 60/085,131
FRIOR FILING DATE: 1998-06-30
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-07-02
FRIOR FILING DATE: 1998-07-02
FRIOR FILING DATE: 1997-07-02
FRIOR FILING DATE: 1997-07-02
FRIOR FILING DATE: 1997-07-02
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Sequence 29866, Application US/09252991A
Sequence 29866, Application US/09252991A
Sequence 29866, Application US/09252991A
Father No. 6551795
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29866
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Best Local Similarity 50.0%; Pred. No. 55;
Matches 11; Conservative 2; Mismatches
                                                  248 VVŠEWITEQĠSWQEIQEKAVEVATVVIQP 276
           2 LISPWIISSGLWPRLQ-KAAEAFKQLNQP 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-583-110-5129
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; Sequence 12, Application US/09881710
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29866
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US-09-252-991A-29866
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US-09-583-110-5129
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LENGTH: 361
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RESULT 13
US-09-252-991A-20461

US-09-252-991A-20461

Sequence 20461, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PLIANTON NUMBER: US 60/094,190

PRIOR PRIOR PLIANTON NUMBER: US 60/094,190

PRIOR PLIANTON NUMBER: US 60/094,190

PRIOR PLIANTON NUMBER: US 60/094,190
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 68
; OTHER INFORMATION: Xaa=Asp or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 69
; OTHER INFORMATION: Xaa=Ala or Asp or His or Asn or Pro or Ser or Thr or US-09-513-999C-7233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09187999A
Patent No. 6482646
BATEN LINGOMATION:
APPLICANT: Gindullis, Frank
APPLICANT: Gindullis, Frank
APPLICANT: Maier, Iris
TITLE OF INVENTION: Proteins that Interact with Nuclear Matrix
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REFERENCE: CL-1321
CURRENT APPLICATION NUMBER: US/09/187,999A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
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                                                                                                                                                                                                                                                                              Length 84;
                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                           Query Match 30.3%; Score 47; DB 4; Best Local Similarity 35.3%; Pred. No. 11; Matches 6; Mismatches 5
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US-09-187-999-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20461
                                                                                                                                                                                                                                                                                                                                                                                                                             30 WPRINSATGQYQRMNKP 46
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US-09-187-999-2
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TYPE: PRT
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US-09-881-710-1
US-09-881-710-1
Sequence 1, Application US/09881710
Factor No. 6673895
GENERAL INFORMATION:
APPLICANT DESPRES, Phillipe
APPLICANT DESPRES, Vincent
APPLICANT CATTEAU, Adeline
APPLICANT CATTEAU, Adeline
TILLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
FILE REFERENCE: 2096-71150
CURRENT APPLICATION NUMBER: US/09/881,710
CURRENT PILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: 60/212,129
FRIOR APPLICATION NUMBER: 60/212,129
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
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; Sequence 723, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Dunas Mine Edwards, J.B.
APPLICANT: Dunas Mine Edwards, J.B.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.;
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.;
FILE REPERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; PRIOR PPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 7233
; LENGTH: 84
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                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
  CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION UNMBER: 60/212,129
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                    3 TSPWTTSSGLWPRLQK 18
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52 TETWMSSEGAWKQIQK 67
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.88
Matches 7; Conservative
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; ORGANISM: Dengue virus
US-09-881-710-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO 1
LENGTH; 76
TYPE: PRT
ORGANISM: Dengue virus
US-09-881-710-1
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ORGANISM: Homo sapiens
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US-09-513-999C-7233
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RESULT 15

US-09-252-991A-25179

i Sequence 25179, Application US/09252991A

i Patent No. 6551795

i GENERAL INFORMATION:

i APPLICANTY MARCY J. RUBenfield et al.

i TILLE OF INVENTION:

I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

I TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

i PRIOR FILING DATE: 1998-02-27

i NUMBER OF SEQ ID NOS: 33142

i LENGTH: 210

i TYPE: PRT

CORGANIEM: PREUDOMORAS AERUGINOSA

US-09-252-991A-25179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.3%; Pred. No. 34;
Matches 11; Conservative 2; Mismatches 7; Indels
5 PWITSSGLWPRLOKAAEA 22
                                21 PMTTSFSIWPPTQRTRDA 38
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> 3 TSPWTTSSGLWPR-----LQKAAEA 22 : ||| | | | | : || 16 SGPWTRRSGSWIRAGRCAVTPLQPSCEA 43

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RESULT 2
US-10-296-115-1110
S-10-296-115-1110
Sequence 1110, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-092-750-36
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4 8 .5
7 . 8 .5
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Sequence 40845, A
Sequence 193474,
Sequence 233344,
Sequence 241808,
Sequence 241808,
Sequence 241908,
Sequence 1179, Ap
Sequence 31025,
Sequence 31025,
Sequence 31025,
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                                                                                                                             November 10, 2004, 16:36:12; Search time 31.1537 Seconds (without alignments) 328.807 Million cell updates/sec
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| cgn2_6/prodata/1/pubpaa/US07 FUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US06_MEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US06_MEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/prodata/1/pubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-767-1110
US-10-767-701-4045
US-10-437-963-193444
US-10-437-963-193444
US-10-4437-963-192472
US-10-4425-115-233344
US-10-408-7654-1179
US-10-408-765A-1179
US-10-408-765A-1179
US-10-108-260A-3910
US-09-775-803-12
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155
1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQP 29
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Match Length DB
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Sequence 63, Appl
Sequence 344373,
Sequence 25426, A
Sequence 15190,
Sequence 17190,
Sequence 17190,
Sequence 1271, A
Sequence 277, Appl
Sequence 277, Appl
Sequence 12917,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 192804,
Sequence 193, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
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Sequence 29, Appl
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Sequence 20, Appl
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US-10-080-334-228
US-10-037-417-105
US-10-781-5963-171554
US-10-425-115-344373
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US-10-425-115-3563
US-10-425-115-357631
US-10-424-599-167199
US-10-424-599-16866
US-10-424-599-168666
US-10-424-599-17017
US-10-431-213-13
US-09-881-710-30
US-09-881-710-38
US-09-881-710-38
US-09-881-710-38
US-09-881-710-38
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US-10-634-895-1
US-10-425-115-189993
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US-10-022-750-36

Sequence 36, Application US/10092750

Sequence 36, Application US/10092750

Publication No. US2030033157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Ualia

TILLE OF INVENTION: Polypeptides Interactive with BCL-XI

FILLE REFERENCE: 50034/050002

CURRENT APPLICATION NUMBER: US/10/092,750

PRIOR APPLICATION NUMBER: US 60/274,526

PRIOR PILIAGION NUMBER: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PASSEE for Windows Version 4.0

SEQ ID NO 36

LENGTH: 29
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Best Local Similarity 100.0
Matches 29; Conservative
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ILTSPWTTSSGLWPRLQKAAEAFKQLNQP 29

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Gaps

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Branzazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
SEQ ID NO 192472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 53; DB 16; Length 460; ilarity 43.5%; Pred. No. 74; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                            Length 600;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_89609C.1.pep
US-10-437-963-193474
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US-10-437-963-192472
                                                                                                                                                                                                                                                         Score 55; DB 1; Pred. No. 52; 1; Mismatches
                                                                                                                                                                                                                                                            Query Match
35.5%; Score 55;
Best Local Similarity 58.8%; Pred. No.
Matches 10; Conservative 1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 192472, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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     CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 193474
LENGTH: 600
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                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 10; Conserv
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US-10-437-963-192472
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBUCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40845, Application US/10767701

Sequence 40845, Application US/10767701

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yondae
APPLICANTON: David K.
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535) B
CURRENT APPLICATION NUMBER: 105/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40845
LENGTH: 259
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APPLICANT: Hyseq Inc
TILE REFERENCE: 784PCT
CURRENT FILING DATE: 2002-11.18
PRIOR APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11.18
PRIOR APPLICATION NUMBER: US/9/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1110
LENGTH: 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10916_1.pep
US-10-767-701-40845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 14; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SPWTTSSGLWPRLQKA 19
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-296-115-1110
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US-10-767-701-40845
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US-10-425-115-233344

i Sequence 223344, Application US/10425115

i Sequence 223344, Application US/10425115

i Publication No. US20040214272A1

i GENERAL INFORMATION:

i APPLICANT: La Rosa, Thomas J.

APPLICANT: Shou, Yahua

i APPLICANT: Thou, Yahua

i APPLICANT: Cao, Yongwai

i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

I TITLE OF INVENTION: Plants

i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

CURRENT APPLICATION NUMBER: US/10/425,115

i CURRENT APPLICATION NUMBER: US/10/425,115

i NUMBER OF SEQ ID NOS: 369326

i SEQ ID NO 233344

i LENGTH: 123
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.9%; Score 51; DB 14; Length 793; 36.0%; Pred. No. 2.5e+02; ive 6; Mismatches 10; Indels
                  Score 51, DB 17; Length 175; Pred. No. 52; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HELIXENSTAND NO. US20030236392A1e1 full length cDNA FILE REPERENCE: H1-A0105 CURRENT PELIXE DATE: US/10/104,047 CURRENT FILIXE DATE: 2002-03-25 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PELIXED DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4096 SOFTWARE: PREOR FLING DATE: 2.1 SEQ ID NO 2549
                                                                                                                                                                                                      7 TTSSGLWPRL-------OKAAEAFKQLNQP
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32.9%; Score 51; DB 16;
Best Local Similarity 36.0%; Pred. No. 6.8e+02;
Matches 9; Conservative 6; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-10-104-047-2549
; Sequence 2549, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
                  Query Match
Best Local Similarity 29.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.0.
These 9; Conservative
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US-10-104-047-2549
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; Sequence 8143, Application US/10369493
; Publication No. US2030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Galdman, Barry S.
TITLE OF INVENTION: EARRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; RIJNG DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8143
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US-10-425-115-241808

Sequence 241808, Application US/10425115

Publication No. US20040214272A1

GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
FILE REFERENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 241808

LENGTH: 175
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33.5%; Score 52; DB 14; Length 531;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                 Length 123;
                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Clone ID: MRT4577_152107C.1.pep US-10-425-115-241808
                                            ; OTHER INFORMATION: Clone ID: NRT4577_144402C.1.pep
US-10-425-115-233344
                                                                                                                                                                 Query Match 33.5%; Score 52; DB 17;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(175)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 PWITSLGYYGMPEKTAEAWRNL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PWTTSSGLWPRLQKAAEAFKQL 26
                                                                                                                                                                                                                                                                                                                                                            52 PWTPKNGLGGWPRFPKKA 69
                                                                                                                                                                                                                                                                                                         5 PWITSSGL--WPRLOXAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i LENGTH: 531
; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-369-493-8143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-369-493-8143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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; LENGTH: 566
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-803-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 301225, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yunual
APPLICANT: Applicant Rovalic, David K.
APPLICANT: Applicant Rovalic, David K.
APPLICANT: Shou, Yihual
ITILE OF INVENTION: Plants
TILLE OF INVENTION: Plants
FILE REPERENCE: 30-21 (5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 301225
LENGTH: 108
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Publication No. US20030167487A1
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Pillips, David
APPLICANT: Prillips, Transgenic Animals Having a Modified Glycoprotein V
TITLE OF INVENTION: Gene and Methods for Their Use
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
ITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFRENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.3%; Score 50; DB 15; Length 264; Best Local Similarity 37.0%; Pred. No. 1.1e+02; Matches 10; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 108; 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_37793C.1.pep
US-10-425-115-301225
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(108)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 PWTRAAAWWGRLEGAKASAKGEQVRDP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.3%; Score 50;
52.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PWTTSSGLWPRLQ - KAAEAFKQLNQP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TSPWITSSGLWPRLOKA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TIPITISRMWPMRQSA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / ORGANISM: Homo sapiens
US-10-108-260A-3910
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-108-260A-3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-775-803-12
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APPLICANT: Gerlach, Valerie
APPLICANT: Spaderna, Steven K
APPLICANT: Zerhusen, Bryan D
APPLICANT: Zerhusen, Bryan D
ATTLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
PILE REFERENCE: 21402-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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CURRENT APPLICATION NUMBER: US/09/775,803
CURRENT FILING DATE: 2001-02-05
PRIOR PEPLICATION NUMBER: CT/US99/17594
PRIOR PELOR PILING DATE: 1999-08-04
PRIOR PILING DATE: 1999-08-04
PRIOR PILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/10/080,334
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/321,712
PRIOR PLILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-13
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-26
PRIOR PELING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-604
PRIOR FILING DATE: 2001-03-604
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/21,521
PRIOR APPLICATION NUMBER: 60/31,595
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR PRILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 228, Application US/10080334
Publication No. US20040002584A1
GENERAL INFORMATION:
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Padigaru, Muralidhara
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pena, Carol E. A.
APPLICANT: Shimkets, Richard A
APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Furtak, Katarzyna
Tchernev, Velizar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vernet, Corine A. Malyankar, Uriel M
Guo, Xiaojia
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Casman, Stacie J
Boldog, Ferenc L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 NPWLCDCGLWPFLQ 434
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Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SPWITSSGLWPRLO 17
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Best Local Similarity 57.1<sup>s</sup>
Matches 8; Conservative
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Pred. No. 2.4e+02;
1; Mismatches 5; Indels
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Ur, Raymond U
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-09-20
PRIOR PAPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR BILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/274,295
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/218,526
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-04-25
PRIOR PELLON NUMBER: 60/286,548
PRIOR PELLON NUMBER: 60/291,765
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/270,797
PRIOR PILING DATE: 2001-03-16
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US-10-037-417-105
Sequence 105, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patturajan, Meera
Grose, William M
Lepley, Denise M
Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tcherney, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ellerman, Karen
Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorman, Linda
Bdinger, Shlomit R
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.3%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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Guo, Xiaojia
Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-080-334-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SPWITSSGLWPRLQ 17
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model protein search, OM protein

November 10, 2004, 12:29:32; Search time 6.46114 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-36 155 1 ILTSPWTTSSGLWPRLQKAABAFKQLNQP 29 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	spos	two-component sens	hydroxymethylbilan	probable enzyme Z2	probable enzyme [i	biotin biosynthesi	probable periplasm	egg membrane, prote	thetical	_		hypothetical prote	e	hypothetical prote	conserved hypothet	phosphoprotein pho	hypothetical prote	polyprotein(C, E,	genome polyprotein	genome polyprotein	genome polyprotein		epidermal growth f		hypothetical prote	probable transcrip	prote	cal	al
od i vidinio o	QI	3698	A12255	IBEG	C85723	F90894	B64906	AI0163	S52847	H71535	T49721	F90602	T37923	D95106	G83536	H81690	S41854	T49265	A47311	C32401	B32401	A32401	839983	I38728	Ž	259	H82983	4221	T51548	515
	DB	!								7																				
	Length	וא	401	480	252	252	252	378	424	698	831	454	688	361	450	253	281	441	775	792	792	792	821	822	1226	1-	305	466	599	103
*	Query Match	· N	$^{\circ}$	32.3	Н	31.6	Η.	Ξ.	1.	31.6	31	31	-1	0	0	0	0	0	0	0	0	О	0	0	0	0	0	0	0	29.7
	Score	.50	20	20	49	49	49	49	49	49		48	48	•	47.5	47	47	47	47	47	47	47	47	47	47	47	46.5	46.5	9	46
	Result No.	;	7	m	4	Ŋ	9	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote probable V-ATPase,	probable glucarate probable glucarate	probable exonuclea hypothetical prote	hypothetical prote	glucarate denydrat probable acvicos	hypothetical prote	glucoamylase [impo	ď.	membrane alanyl am	glycine cleavage s	ın.	protein A - flock
F84716 T47216	H91084 A85930	AG2363 F72089	F86534	H65060	F98136	AE3151	AH0437	A53984	AG2381	QQBBB1	S41397
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4 6 4 6	4.4 6.4	46 46	46	46	4 4 6 9	46	46	46	46		46
3 3 3	3.52	ა ი 4 ი	36	37	20 CM	40		42	43	44	45

ALIGNMENTS

	RESULT 1
	T36983
	probable transposase - Streptomyces coelicolor
	C;Species: Streptomyces coelicolor
	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
	C; Accession: T36983
	R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
	submitted to the EMBL Data Library, August 1999
	A; Reference number: Z21618
	A;Accession: T36983
	A;Status: preliminary; translated from GB/EMBL/DDBJ
_	A; Molecule type: DNA
	A; Residues: 1-282 < OLI>
	A; Cross-references: UNIPROT: Q9R192; EMBL: AL109949; PIDN: CAB52897.1; GSPDB: GN00070; SCOE
	A; Experimental source: strain A3(2)
	C, Genetics:
	A, Gene: SCOEDB:SCJ11.12
	C, Superfamily: Streptomyces coelicolor probable transposase SC6G9.36C
	Ouery Match 32.3%; Score 50; DB 2; Length 282;
	Best Local Similarity 53.3%; Pred. No. 16; Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
	OY 3 TSWITTSGLWPKLO 1 /
	Db 16 TSPWINSDELWDRVE 30
	RESULT 2

SCOEDE

ALZ255
two-component sensor histidine kinase all3600 [imported] - Nostoc sp. (strain PCC 7120)
C;Specides: Nostoc sp. PCC 7120
C;Specides: Nostoc sp. PCC 7120
C;Specides: Nostoc sp. pcC 7120
C;Specides: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: ALZ255
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: Al2255
A;Accession: Al2255
A;Accession: Al2255
A;Accession: Al2255
A;Accession: Al2255
A;Coss-references: UNIPROT: Q8YRSO; GB:BA000019; PIDN:BAB75299.1; PID:G17132733; GSPDB:GNA;Cene: al13600
C;Genetics: al13600
C;Genetics: al13600
C;Superfamily: sensory transduction system regulatory protein homolog

32.3%; Score 50; DB 2; Length 401; 40.9%; Pred. No. 23; Query Match Best Local Similarity

Mismatches

Conservative

9.

Matches

7 TTSSGLWPRLQKAAEAFKQLNQ 28

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R;HHYASHI, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A)NA Res. B, 11-22, 2001

A)NA Res. B, 11-22, 2001

A)Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; WUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: B64906
R;Blattner, F:R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A;Itle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64906
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Affile: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 «HAX>
A;Cross-references: UNIPROT:Q8XAZ2; GB:BA000007; PIDN:BAB35549.1; PID:g13361592; GSPDB:GN-A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P76145; GB:AE000249; GB:U00096; NID:g1787790; PIDN:AAC74592.1
A,Experimental Source: Strain K-12, Substrain MG1655
C;Superfamily: bloc protein; bioc homology
F;32-130/Domain: bloc homology <BIOC>
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                                                                                                   - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
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                                                                                                                                     C,Species: Escherichia coli
C,Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C,Accession: F90894
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C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B64906
biotin biosynthesis protein homolog b1519 - Escherichia coli (strain K-12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 252;
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Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.6%; Score 49; DB
llarity 47.6%; Pred. No. 19;
Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ECs2126
C;Superfamily: bioC protein; bioC homology
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                                                                                                       probable enzyme [imported]
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                    hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Euglena gracilis
N'Alternate names: porphobilinogen deaminase; pre-uroporphyrinogen synthase
C;Species Euglena gracilis
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S06109
R;Sharif, A.L.; Smith, A.G.; Abell, C.
Bur. J. Blochem. 184, 353-359, 1989
A;Title: Isolation and characterisation of a cDNA clone for a chlorophyll synthesis enzy
h;Reference number: S06109; WUID:90005485; PMID:2477247
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-252 < <870>
A;Cross-references: UNIPROT:Q8XAZ2; GB:AE005174; NID:g12515147; PIDN:AAG56247.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
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***Perna**, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
**Nature 409, 529-533, 2001
**A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
**A;Title: Genome sequence of A;Reference number: A85480; MUID:21074935; PMID:11206551
**A;Accession: C85723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Description: catalyzes the stepwise polymerization of four molecules of porphobilinoge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Pathway: porphyrin biosynthesis
A, Note: acting with uroporphyrinogen III synthase (cosynthase), which cyclizes hydroxyme.
C, Superfamily: hydroxymethylbilane synthase
C, Keywords: ammonia-lyase; carbon-nitrogen lyase; chlorophyll biosynthesis; chloroplast; p; 1-139 f Domain: transit peptide (chloroplast) #status predicted <TNP:
F, 140-480/Parduct: hydroxymethylbilane synthase #status experimental <AMT>
F, 395/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1480 <SHA>
A;Cross-references: UNIPROT:P13446; GB:X15743; NID:g18411; PIDN:CAA33759.1; PID:g18412
A;Note: part of this sequence, including the amino end of the mature protein, was confit
A;Note: 175-Ala was also found
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable enzyme Z2186 [imported] - Bscherichia coli (strain O157:H7, substrain EDL933)
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
Gaps
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   9
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Query Match 32.3%; Score 50; DB 1; Best Local Similarity 55.6%; Pred. No. 28; Matches 10; Conservative 2; Mismatches 4

5 PWTTSSGLWPRLQKAAEA 22

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31.6%; Score 49; DB 2; larity 47.6%; Pred. No. 19; Conservative 4; Mismatches 7

Query Match Best Local Similarity Matches 10; Conserv

Best Loca Matches

C, Superfamily: bioC protein; bioC homology

C;Genetics:

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-688 <CON>
A;Cross_references: UNIPROT;Q10109; EMBL:Z68198; PIDN:CAA92388.1; GSPDB:GN00066; SPDB:SP?
A;Experimental source: strain 972h-; cosmid c18G6
C;Genetics:
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-213, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUD:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aminopeptidase (leucine aminopeptidase) (lap) [imported] - Mycoplasma pulmonis (strain U?
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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                                   Cispecies: Neurospora crassa
Cispecies: Neurospora crassa
Cispecies: Neurospora crassa
Cispecies: Neurospora crassa
Ciscomit 1927.1
Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 2250.2
A;Reference number: 2250.2
A;Accession: T49721
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-831 cSCH>
A;Cross-references: UNIPROT: 099535; EMBL:Al356172; GSPDB:CN00116; NCSP:B23L21.340
A;Experimental source: BAC clone B23L21; strain OR74A
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hypothetical protein B21121.340 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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31.6%; Score 49; DB 2; Length 831;
Best Local Similarity 38.1%; Pred. No. 73;
Matches 8; Conservative 5; Mismatches 8; Indels
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6; Mismatches
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Pred. No.
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770 LLTSPSPAEKALWPKFEEMAK 790
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A,Gene: MYDU 7260
A,Genetic code: SGC3
C,Superfamily: Cytosol aminopeptidase
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Best Local Similarity 36.8%;
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-454 <KUR>
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A;Gene: NCSP:B23L21.340
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C,Species: Chlamydia trachomatis
C,Accession: H71535
R,Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 74-759, 1998
A,Fite: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, Reference number: A71570; MUD:99000809; PMID:9784136
A,Rocession: H71535
A,Rocession: H71535
A,Rocession: H71535
A,Rocession: H71535
A,Rocession: H71535
A,Rocession: H71535
A,Stephens: DAA
A,Rocession: H71535
A,Stephens: DAA
A,Rocession: H71535
A,Stephens: DAA
A,Rocession: DAA
A,Rocession: C7283
C,Genetics:
C,Superfamily: Chlamydia trachomatis hypothetical protein C7283
                      A;Molecule type: DNA
A;Residues: 1-378 «XUR»
A;Cross-references: UNIPROT:Q8ZGF8; GB:AL590842; PIDN:CAC90172.1; PID:g15979391; GSPDB:G
C;Genetics:
A;Gene: YP01343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-424 cCHA>
A, Rossidues: 1-424 cCHA>
A, Cross-references: UNIPROT. Q92027, EMBL. 248972, NID. 9763077, FIDN. CAA88836.1, FID. 97630
C, Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology
F,110-364/Domain: ZP domain homology cZPH>
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C;Species: Cyprinus carpio (common carp)
C;Date: 09-Unn-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: $52847
B;Chang, Y: Wang, S:; Tsao, C.; Huang, F.
Submitted to the EMBL Data Library, April 1995
A;Rescription: Structural analysis and expression of carp ZP3 gene.
A;Accession: $52847
A;Accession: $52847
A;Accession: $52847
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                                                                                                                                                                                                                         Query Match 31.6%; Score 49; DB Best Local Similarity 39.1%; Pred. No. 30; Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.6%; Score 49; DB Best Local Similarity 45.0%; Pred. No. 34; Matches 9; Conservative 4; Mismatches
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Best Local Similarity 33.3
Matches 10; Conservative
                   A;Status: preliminary
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δ d RESULT 10 T49721

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A;Cross-references: UNIPROT:Q9PKB1; GB:AE002323; GB:AE002160; NID:g7190585; PIDN:AAF39395; A;Experimental source: strain Nigg (MoPn) C;Genetics:
                                                                                                                      conserved hypothetical protein frameshift TC0556 [imported] - Chlamydia muridarum (strair
                                                                                                                                                                                                                                        R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                          Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SPWITSSGLW----PRLQKAAEAFKQLNQP 29
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ne: 7.46114 secs
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Pred. No. 3
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Best Local Similarity 33.3%;
Matches 10; Conservative 7
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A;Molecule type: DNA
A;Residues: 1-253 <TET>
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Cjaceis: Streptococcus pneumoniae
Cjaceis: Streptococcus pneumoniae
Cjaceis: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
Cjaceis: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
Cjaceis: D5106
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A;Title: Complete genome sequence of Pseudomonas acruginas PA01, an opportunistic pathorance number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: Draminary
A;Residues: L450 csTO>
A;Residues: UND:2043737; PMID:10984043
A;Cross-references: UNIPROT:Q91564; GB:AE004522; GB:AE004091; NID:g9946768; PIDN:AAG0427
C;Genetics:
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44.4%; Pred. No. 60;
                                                                                                                 Length 688;
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A;Gene: SP0921
C;Superfamily: uncharacterized conserved protein SP0921
                                                                                                                 Score 48; DB 2;
Pred. No. 82;
2; Mismatches
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A;Gene: SPDB:SPAC18G6.10
A;Map position: 1
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Matches 12; Conserv
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Gaps 4.

6

Mismatches

Length 253; Indels

DB 2;

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November 10, 2004, 12:27:34; Search time 35.4111 Seconds (without alignments) 471.205 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                             OM protein - protein search, using sw model
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US-10-092-750-36 155 1 ILTSPWTTSSGLWPRLQKAABAFKQLNQP 29 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
No.	Score	e Match	Length	DB	ID	De
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ΙD	Q91VT7	639н6Ф	Q99K30	бэн623	Q72BM7	AAS96086	Q6ZUB3	BAC86313	Q7R724	Q81W90	AAT33212	62TDZ6	Q7U758	Q8SV18	Q88BA1	03880	0993н6	OESLB9	AAR30119		CHD6_HUMAN	Q7VSC4	Q7WKB7	Q8N816	Q9RI92	Q8YR50	Q8XYA8	HEM3_EUGGR	Q8LJA3	GPV RAT	<u>0</u> 90 <u>z</u> u3
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Q9WT88 Q7SAD6	Q61X33 AAT37495	027072	Q7S925 O6X115	AAR10040	Q6XJ13	O9W3W8	AAR09689	Q7PUX3	TAM ECO57	TAM_ECOLI
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32 33	3 3 5	36	37	6.6	40	41	42	43	44	45

ALIGNMENTS

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TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
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WEDLINE=22503195; PubMed=12620401;
MEDLINE=22503195; PubMed=12620401;
MINISTRATION CONFAILONINE ST. Scita G., Di Fiore P.P., Betsholtz C.;
Transitico analysis of the EPS8 gene family: genomic organization,
Transcalon profile, and protein structure.";
MEMBL; AK025824; BAB15248.1; -.
REMBL; AK026020; PTE_PID.
RICEPPRO; IPR001036; PH related.
RICEPPRO; IPR001036; PH related.
RICEPPRO; IPR001045; SH3.1; -.
REMBL; PS00018; SH3.1; -.
REMBL; PS00018; SH3.1; -.
REMBL; PS00179; PID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Watanabe K., Kumagal A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Epidermal growth factor receptor pathway substrate 8-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ22171 (Epidermal growth factor receptor pathway substrate 8 related protein 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          715 AA; 80620 MW; DAB07744B04CFEE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.2%; Score 67; DB 2;
100.0%; Pred. No. 1.2;
rative 0; Mismatches (
                                                                                                                                                                      715 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                   PRT;
                                                        275 RLOKAAEAFKOLNO 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 RLQKAAEAFKOLNO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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SEQUENCE FROM N.A.
STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q99K30;
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DT 01
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NEDLINE=22388257; PubMed=1247732;

A KINDLINE=22388257; PubMed=1247732;

A Litasher R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garrian S., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Bahesley W., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okawabata A., Hikiji T., Kobatake N., Inagaki H., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO25589; BAB15180.1; -.
HSSP; QOB509; 110C.
Genew; HGNC:21296; EPS8L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005492; AAH05492.1; -.
HSSP, Q08509; 110C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82229 MW; A11DE82FF2C0BD18 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein FL721935.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.2%; Score 67; DB 2;
100.0%; Pred. No. 1.2;
iive 0; Mismatches
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GO, GO:0004872; F:receptor activity; IEA.
InterPro; IPR010108; PH related.
InterPro; IPR00105; PH PE ID.
InterPro; IPR00145; SH3.
Fram; PR00018; SH3.
Probom; PD000006; SH3.1; 1.
SYMART; SM00226; SH3; 1.
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PROSITE; PS50002; SH3; 1.
Receptor; SH3 domain.
SEQUENCE 729 AA; 82229
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Matches 14; Conservative
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Q9H6S3
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NCBI_TaxID=9606;
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AAS96086;
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Q6ZUB3;
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P. PEDUBROLE FROM N.A.

P. PUDMEG-15077118; DOI-10.1038/nbt959;

Reidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,

A. Daugherty S.C., DeBoy R.T., Mard N.L., Merhe B.A., Brinkac L.M.,

Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,

A. Daugherty S.C., BeBoy R.T., Dodson R.J., Durkin A.S., Madupu J.,

Daugherty S.C., Bance M.Y. Zafar N., Zhou L., Selengut J.,

Daugherty S.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Despective M. T. D., Voordouw G., Fraser C.M.;

The genome sequence of the anaerobic, sulfate-reducing bacterium

Desulfovibrio vulgaris Hildenborough.";

The genome sequence of the anaerobic, sulfate-reducing bacterium

The genome sequence of the anaerobic,

The genome sequence of the anaerobic,

Interporium T. V., Wall J.D., Voordouw G., Fraser C.M.;

The genome sequence of the anaerobic,

Interporium T. V., Wall J.D., Voordouw G., Fraser C.M.;

The genome sequence of the anaerobic, sulfate-reducing bacterium

The genome sequence of the anaerobic,

The genome sequence of the anaerobic,

Interporium T. V., Wall J.D., Voordouw

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The genome sequence of the anaerobic sequence of the ana
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Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 2; Length 743;
Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                               743 AA; 83792 MW; DB01D8F6363A1F80 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DNA ligase, NAD-dependent (EC 6.5.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 43.2%; Score 67; DB Similarity 100.0%; Pred. No. 1.2 14; Conservative 0; Mismatches
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InterPro; IPR004149; Znf_DNAligase_C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF03120; DNA_ligase_OB; 1.
Pfam; PP03119; DNA_ligase_ZBD; 1.
Pfam; PF00633; HHH; 1.
InterPro; IPR011036; PH related.
InterPro; IPR006020; PTB_PID.
InterPro; IPR00145; SH3_F1D.
Ffam; PP00018; SH3_1; 1.
ProDom; PD000066; SH3; 1.
SMART; SW0326; SH3; 1.
PROSITE; PS01179; PID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 RLOKAABAFKOLNO 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             SH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio. VCBI_TaxID=882;
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05-JUL-2004 (TYEMBLrel. 27, Last sequence update)
05-JUL-2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43854.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2004 (TrEMBLrel. 27, Created)
27-APR-2004 (TrEMBLrel. 27, Last sequence update)
27-APR-2004 (TrEMBLrel. 27, Last annotation update)
DNA ligase, Nab-dependent (EC 6.5.1.2).
LIGA OR DVU1608.
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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0
                                                                                         SMART; SM00532; LIGANC; 1.
TICRFAMS; TIGR00575; dnlj; 1.
PROSITE; PS50172; BRCT; 1.
PROSITE; PS101056; DNA_LIGASE_N2; 1.
COMplete proteone; DNA_repair; DNA_replication; Ligase; NAD.SEQUENCE 799 AA; 86098 WW; 535A6009B6B60EA3 CRC64;
                                                                                                                                                                                                                                                                                                             36.1%; Score 56; DB 2; Length 799; 62.5%; Pred. No. 48; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.1%; Score 56; DB 2; Length 799; 62.5%; Pred. No. 48; ive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             799 AA
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ProDom; PD003944; DNAligase;
SMART; SM00292; BRCT; 1.
SMART; SM00278; HHH1; 3.
SMART; SM00532; LIGANC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TSPWTTSSGLWPRLQK 18
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                                                                                                                                                                                                                                                                                                                                               Local Similarity 62.5%;
les 10; Conservative
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les 10; Conservative
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Hypothetical protein (Fragment).
Name=PY07765;
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                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                NCBI_TaxID=73239;
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                                                                                                      PubMed=12368865;
                                                                                           STRAIN=17XNL
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NON TER
SEQUENCE
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Q81W90
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                   Cota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T., Chisbur-Teselis.

A Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,

Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,

Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,

Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,

Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,

Masubo Y., Nagai K., Isogai T.,

Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AK12542; BAC66313.1;

InterPro; IPR001194; DENN.

InterPro; IPR001194; DENN.

InterPro; IPR001194; DENN.

Pfam; PF01455; dDENN; 1.

Pfam; PF01535; PRF.;

Pfam; PR05114; DENN; 1.

RROSITE; PSS0947; DDENN; 1.

RROSITE; PSS0947; DDENN; 1.
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"NEDO human cDNA sequencing project.";
Submitted (JUL 2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK125642; BAC86313.1.
                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                          Length 1557;
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                                                                                                                                                                                                                                                                                                    Indels
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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513 VLESPWPSSTRSGIFLWTKVRNVVRGLAOFROP 545
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513 VLESPWPSSTRSGIFLWTKVRNVVRGLAQFRQP 545
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1557 AA
                                                                                                                                                                                                                                                                                                                               1 ILTSPW--TTSSG--LWPRLQKAAEAFKQLNQP
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ses 12; Conserv
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TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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01-MAR-2004 (
01-MAR-2004 (
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Q7R724;
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Matches
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Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Shellom S.J., van Aken S.E., Shumaway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
A. Florens L., Yares F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.W. Bergman L.W., Valdya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
A. Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Genome sequence and comparative analysis of the model rodent malaria
T. parasite Plasmodium yoelii yoelii.";
Darasite Plasmodium yoelii yoelii.";
EMBL/GenBankDDBJ whole genome shotgun (WGS) entry which is.
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SEXAMELER FOR M.A.

STRAINE-ADER (1solate Porton),

STRAINE-ADER (1solate Porton),

Read T.D., Peterson S.N., Toursase N.J., Baillie L.W., Paulsen I.T.,

A Read T.D., Peterson S.N., Toursase N.J., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinker L.M., Gwinn M.L.,

A Rolson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

Razen A., Cline R.T., Redund C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Haran P.C., Kolstoe A.-B., Fraser C.M.;

The genome sequence of Bacillus anthracis Ames and comparison to

closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
pamorioni yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 54; DB 2; Length 707; 50.0%; Pred. No. 82; ive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707 707 AA; 77054 MW; DC40A56BA854AEFB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
EMBL, AABL01002913; EAA20293.1; -.
Hypothetical protein.
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STRAIN=Ames / isolate 0581;
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Best Local Similarity 50.0
Matches 10; Conservative
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Nature 423:81-86(2003)
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Mimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio M., Harsahi M., Ando T., Aoki H., Arita K., Hamada M., Harsahi M., Ramada C., Ramoro M., Itoh S., Itoh T., Itoh Y., Idonuma A., Iijima M., Ikeda M., Rarasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machira K., Machara T., Mixuno H., Mizubayashi T., Mukai Y., Nakamira M., Negishi M., Oha I., Ono N., Saji S., Sakai, K., Shibata M., Andong H., Namagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Itama H., Rado T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., Yuka Yano M., Jiang J., Gojobori T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., The genome sequence and structure of rice chromosome I.";
           Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0699D11 (Similar to Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence).
                                                                              oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; NTATATOLIOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; Poales; Poaceae; NTATATOLIOPHYTA; POACEAE; POACEAEE; POACEAE; POACEAE
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SEQUENCE 460 AA; 48759 MW; 33BA11150391880B CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro; IPR003480; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein precursor.
OrderedLocusNames=SYNW1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP002817; BAB03452.1; -. EMBL; AP001366; BAA92409.1; -. EMBL; AP001366; BAA92405.1; -.
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nes 10; Conserv
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Matches
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Federova N.B.,
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B. Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M. "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017334; AAT33212.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                               ., Hill K.,
Okinaka R.
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%; Score 53; DB 2; Length 251; 35.7%; Pred. No. 39; sive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%; Score 53; DB 2; Length 251; 35.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                               8; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
Bacillus cereus group, Bacillus anthracis.
NCBI_TaxID=261594;
                                                                                                          "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0008462; F:endopeptidase Clp activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPRO1907; Pept_S14_ClpP.
Pfam; FPF06574; CLP protease; I.
PRINTS; PR00127; CLPPROTEASEP.
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Last sequence update)
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118 MIHNAWTYASGNADQLRKAADDIERINQ 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ILTSPWTTSSGLWPRLQKAAEAFKQLNQ 28
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01-JUN-2004 (TrEMBLrel. 27, Last seq
01-JUN-2004 (TrEMBLrel. 27, Last ann
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.7*
...hes 10; Conservative
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                   Wilson M., S
Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoul H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozon cuniculi:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SETALN=DC3000,
STRAIN=DC3000,
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
Buell C.R., Joacdar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daudherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Transcriptional regulator, LysR family.
OrderedLousushames=PSPT00116;
Pseudomonas syringae (pv. Lomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0003676; F:nucleic acid binding; IEA.
Interpro; IPR008994; Nucleic_acid_OB.
Hypothetical protein.
SEQUENCE 413 AA, 47285 MW; F0A401A6DDBFFF89 CRC64;
                                                                                                                                                                                                                                                                                                                                       01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ECU05_1050.
Name=ECU05_1050;
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                                                                                                                                                                                                                                                                                         413 AA.
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Best Local Similarity 50.0%; Pred. No. 51; Matches 11; Conservative 2; Mismatches
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                                                                                    6 WITSSGLWPRLOKAAEAFKQLN 27
                                                                                                                                           16 WTTASGMWRSLSDQGSAL-QLN 36
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                     Q8SVI8;
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Q8SVI8
ID Q8SVI
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Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
Bender C.L., White O., Fraser C.M., Collmer A.;
I'The complete genome sequence of the Arabidopsis and tomato pathogen
I'The complete genome sequence of the Arabidopsis and tomato pathogen
I'The complete genome sequence of the Arabidopsis and tomato pathogen
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I'The Complete genome sequence of the Arabidopsis and tomato pathogen
I'The Complete genome sequence of the Arabidopsis interpro; IPR0006119; LysR subst.

Refam; PR01466; HTH LysR subst.
Refam; PR01466; HTH LysR substrate; I.
Refam; PR01466; HTH LysR substrate; I.
Refam; PR01466; HTH LysR substrate; I.
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Complete protecome; DNA-binding; Transcription regulation.
SEQUENCE 306 AA; 34681 MW; BE98F966404F962F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 78;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00039; HTHLYSR PROSITE; PS50931; HTH LYS
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us-10-092-750-37.rai

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Sequence 26717, A Sequence 32786, A Sequence 22121, A Sequence 22121, A Sequence 21479, A Sequence 12479, A Sequence 5, Appli Sequence 43963, A Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 2, Appli Sequence 3, Appli Sequence
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Sequence 3, Appli
Sequence 471, App
                                                                                                            November 10, 2004, 12:32:37; Search time 11.0535 Seconds (without alignments) 191.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
1: /cgTZ_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgTZ_6/ptodata/1/laa/5B_COMB.pep:*
4: /cgTZ_6/ptodata/1/laa/6A_COMB.pep:*
5: /cgTZ_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgTZ_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgTZ_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-270-767-32786
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US-09-252-991A-22121
US-09-252-991A-22121
US-09-253-991A-31679
US-09-253-991A-31679
US-09-543-601A-31679
US-09-568-102-5
US-09-568-102-5
US-09-568-486-5
US-09-568-488-5
US-09-568-488-5
US-09-03-03-11186
US-09-03-03-11186
US-09-03-03-11186
US-08-08-08-08-11186
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1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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US-08-535-837-3
US-09-620-405B-471
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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                                                                                                                                                                                                                                  Sequence:
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No.
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, LOCATION: (87) , OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknov US-09-248-796A-26717

NUMBER OF SEQ ID NOS: 28208; SEQ ID NO S - 26717
LENGTH: 130
TYPE: PRT
ORGANISM: Candida albicans
FRATURE: NAME/KEY: UNSURE

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33.0%; Score 58; DB 4; Length 130; 47.6%; Pred. No. 0.77; tive 5; Mismatches 6; Indels

33.0 Best Local Similarity 47.6 Matches 10; Conservative

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RESULT 2
US-09-770-767-32786
US-09-270-767-32786

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT PEDLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1998-03-17

NUMBER OF SEQ ID NOS: 62517

SOFFWARE: Patentin Ver. 2.0

SEQ ID NO 32786

LENOTH: 312

TYPE: PRT

28	49	27.8	154	4	US-09-433-826B-471	Sequence 471, App
29	49	27.8	154	4	US-09-604-287A-471	471,
30	49	27.8	154	4	US-09-834-759-471	471,
31	49	27.8	154	4	US-09-590-751A-471	471,
32	49	27.8	621	4	US-09-489-039A-13909	
33	49	27.8	1403	N	US-08-694-865-17	
34	49	27.8	1403	m	US-09-124-491-17	
35	49	27.8	1403	4	US-09-383-912-17	
36	48	27.3	39	m	US-09-082-279B-516	
3.7	48	27.3	39	m	US-09-315-304B-516	
38	48	27.3	39	4	US-09-834-784-516	
39	48	27.3	39	4	US-09-515-965A-516	
40	48	27.3	39	4	US-09-350-641C-516	
41	48	27.3	33	4	US-09-350-841A-516	
42	48	27.3	46	4	US-09-621-976-4860	
43	48	27.3	181	4	US-09-252-991A-23315	
44	48	27.3	183	4	US-09-134-000C-4230	4
45	48	27.3	354	4	US-09-270-767-44204	44204, A
					ALIGNMENTS	
RESULT 1						
US-09-248-796A-26717	3-796A-	26717				
; Sequence	te 2671	7, Appl:	ication	US	Sequence 26717, Application US/09248796A	
, Patent	Patent No. 6747137	47137				
, GENERAI	LINFOR	GENERAL INFORMATION:				
; APPLI	ANT: K	APPLICANT: Keith Weinstock et al	instock	et	al	
; TITLE	OF INV	ENTION:	NUCLEI	Z U	TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES	S RELATING TO CANDIDA ALBICANS
; TITLE	OF INV	ENTION:	FOR D	IAG	TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS	
; FILE !	REFEREN	FILE REFERENCE: 107196.132	196.132			
CURRE	T APPL	ICATION	NUMBER	9	CURRENT APPLICATION NUMBER: US/09/248,796A	
; CURREI	AT FILL	CURRENT FILING DATE: 1999-02-12	1999	-02		
; PRIOR	APPLIC	ATION N	UMBER:	as	PRIOR APPLICATION NUMBER: US 60/074,725	
, PRIOR		FILING DATE: 1998-02-13	1998-02	-13		
; PRIOR		ATION N	UMBER:	ΩS	APPLICATION NUMBER: US 60/096,409	
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RESULT 6
US-09-252-991A-31679
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Fatent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: APERICANT APPLICANTION: APPLICANTION APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION NUMBER: US 60/074,788
FRIOR APPLICANTION NUMBER: US 60/074,788
FRIOR PRICE APPLICANTION NUMBER: US 60/074,788
FRIOR PRICE APPLICANTION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
FYEE: PRICE APPLICANTION NUMBER: US 60/094,190
FRIOR FILING DATE: PSEQ ID NOS: 33142
FYEE: PRICE APPLICANTION NUMBER: US 60/094,190
FYEE: PR
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Sequence 48003, Application US/09270767
Sequence 48003, Application US/09270767
GENERAL INFORMATION:
APPLICATIVE HOMBUTGER et al.
TILLE OF INVENTION: Nocleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE PARENTIN Ver. 2.0
SEQ ID NO 48003
LENGTH: 312
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                                                                                                                    DB 4; Length 312;
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Pred. No. 2.9;
1; Mismatches
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Pred. No. 9.9;
1; Mismatches
                                                                                                                                                                                                    1; Mismatches
                                                                                                            Query Match 32.4%; Score 57;
Best Local Similarity 54.2%; Pred. No. 2
Matches 13; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                      185 ÓPTLLLNTIÓHWPÁLHKWLDLNYL 208
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US-09-543-681A-5973
; Sequence 5973, Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 OPRLLONQOQHLPALPIWFLLQWL 27
; ORGANISM: Drosophila melanogaster
US-09-270-767-32786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Drosophila melanogaster
US-09-270-767-48003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.4%;
Best Local Similarity 54.2%;
Matches 13; Conservative
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illarity 48.5%;
Conservative
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Best Local Similarity
Matches 16; Conserv
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 12000-04-05
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICATION
APPLICATIO
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US-09-489-039A-12472
Sequence 12472, Application US/09489039A
Sequence 12472, Application US/09489039A
Sequence 12472, Application US/09489039A
Setent No. 6610816
Patent No. 6610816
Title OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12472
LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.1%; Score 53; DB 4;
Best Local Similarity 37.5%; Pred. No. 14;
Matches 12; Conservative 6; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 KTLAVRMKOHEOSGLE----IARWLKOHPL 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-5973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5973
LENGTH: 398
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Sequence 5, Application US/09568480
; Sequence 5, Application US/09568480
; Patent No. 635548
; GENERAL INFORMATION:
   APPLICANT: Schupp, Thomas
   APPLICANT: Ligon, James
   APPLICANT: Ligon, James
   APPLICANT: Ligon, James
   APPLICANT: Cyr. Devon
   APPLICANT: Cyr. Devon
   APPLICANT: Goerlach, Joern
   TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
   TITLE REFERENCE: 4.30582A
   CURRENT FILING DATE: 1900-05-10
   PRIOR APPLICATION NUMBER: 09/335,409
   PRIOR APPLICATION NUMBER: 09/335,409
   PRIOR SEQ ID NOS: 30
   SOFTWARE: Patentin Ver. 2.0
   SEQ ID NO 5-10
   SEQ ID NO 5-10
   SEQ ID NO 5-10
                                                                                                                                                                                                                  RESULT 10
US-09-567-969-5

j Sequence 5, Application US/09567969

j Patent No. 635547

j GENERAL INFORMATION:
    APPLICANT: Schupp, Thomas
    APPLICANT: Molnar, Istvan
    APPLICANT: Molnar, Istvan
    APPLICANT: Molnar, Istvan
    APPLICANT: Gerlach, Joern
    APPLICANT: Gerlach, Joern
    APPLICANT: Gerlach, Joern
    APPLICANT: GOSTACH, SOSS
    APPLICANT: GOSTACH, SOSS
    APPLICANT: GOSTACH, JOERN
    APPLICANT: MUMBER: 09/335,409
    PRIOR PILING DATE: 1099-06-17
    NUMBER OF SEQ ID NOS: 30
    SOFTWARE: PATENTIN VEY: 2.0
    SEQ ID NO S
    LENGTH 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.3%; Score 51.5; DB 3; Length 7257; Best Local Similarity 41.7%; Pred. No. 6.2e+02; Matches 15; Conservative 4; Mismatches 12; Indels 5
                                                                                        4499 TVDARLVVRQPAGLTPAQAATVPVAFLTAWLALHDL 4534
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// ORGANISM: Sorangium cellulosum
US-09-568-480-5
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Sequence 5, Application US/09568102

Patent No. 6346404

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Goerlach, Joern

TILL OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT FILING DATE: 1999-06-17

FRIOR APPLICATION NUMBER: 09/335,409

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 7257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09335409
; Patent No. 6121029
; Patent No. 6121029
; GENERAL INFORMATION Thomas
; APPLICANT: Ligon, James
; APPLICANT: Ligon, James
; APPLICANT: Ligon, James
; APPLICANT: Zirkle, Ross
; APPLICANT: Zirkle, Ross
; APPLICANT: Goetlach, Joern
; APPLICANT: Goetlach, Joern
; APPLICANT: Goetlach, Joern
; APPLICANT: Goetlach, Joern
; TILE REFERENCE: 4-30582A
; CURRENT APPLICANTION NUMBER: US/09/335,409
; CURRENT APPLICANT: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: PATENTIAL APPLICANTION NUMBER OF SEQ ID NO 5
; LENGTH: PATENTIAL APPLICANTIAL APP
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Pred. No. 6.2e+02;
4; Mismatches 12; Indels 5.
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                                                                                                                                                         DB 4; Length 301;
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                                                                                                                                                                                                                                                                                                           6 RILCNOOCHLPALPIWFLLOWL----RLH 30
                                                                                                                                                     Query Match 29.3%; Score 51.5; D
Best Local Similarity 43.8%; Pred. No. 17;
Matches 14; Conservative 2; Mismatches
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12472
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; ORGANISM: Sorangium cellulosum
US-09-568-102-5
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Best Local Similarity 41.7%;
Matches 15; Conservative
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US-09-335-409-5
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7

Gaps

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GENERAL INFORMATION:
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US-09-270-767-33963
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                 RESULT 12
US-09-568-486-5

Squence 5, Application US/09568486

Patent No. 6355459

GENERAL INFORMATION:

APPLICANT: Schupp, Thomas

APPLICANT: Algon, James

APPLICANT: Algon, James

APPLICANT: Algon, James

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-3058.24

CURRENT APPLICATION NUMBER: US/09/568,486

CURRENT APPLICATION NUMBER: 09/335,409

PRIOR FILING DATE: 2000-05-10

PRIOR FILING DATE: 2000-05-10

PRIOR FILING DATE: 200-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE PATENTING DATE: 2006-05-17

LENGTH PATENTING DATE: 2006-17

LENGTH PATENTING DATE: 2006-05-17

LENGTH PATENTING DATE: 2006-05-10

LENGTH PATENTING DATE: 2006-05-10

LENGTH PATENTING DATE: 2006-05-10

LENGTH PATENTING DATE: 2006-05-10
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Sequence 5, 3pplication US/09568472

Patent No. 6358719

GENERAL INFORMATION:

APPLICANT: Ligon, Thomas

APPLICANT: Molnar, Istvan

APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross

APPLICANT: Zirkle, Ross

APPLICANT: Gerlach, Joern

ITILE OF INVENITON: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/568,472

CURRENT APPLICATION NUMBER: 09/335,409

PRIOR PILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5.

LENGTH: 7257
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CRGANISM: Sorangium cellulosum
US-09-568-486-5
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ORGANISM: Sorangium cellulosum
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RESULT 14 US-09-567-899-5 Sequence 5, Application US/09567899 ; Patent No. 6383787

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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOmburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33963
LENGTH: 135
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr Devon
APPLICANT: Lose Control Control
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33963
                                                                                                                                                                                                                                                                                                                                                                                                                                                ) TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-899-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.3%;
Best Local Similarity 41.7%;
Matches 15; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 527
LENGTH: 7257
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Sequence 271834, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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US-10-092-750-37
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US-10-425-115-271834
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US-10-092-750-37
Query Match
Best Local S
Matches 32
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Sequence 271834,
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 1159, Appl
Sequence 117, Appl
Sequence 451, Appl
Sequence 451, Appl
Sequence 451, Appl
Sequence 451, Appl
Sequence 459, Appl
Sequence 459, Appl
Sequence 459, Appl
Sequence 459, Appl
                                                                                             November 10, 2004, 16:36:12; Search time 34:3765 Seconds (without alignments) 328.807 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PcT_Rew_PUB_Pepp:*

2: /cgn2_6/ptodata/1/pubpaa/PcT_Rew_PUB_Pepp:*

3: /cgn2_6/ptodata/1/pubpaa/BcG_NEW_PUB_Pepp:*

4: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB_Pepp:*

5: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB_Pepp:*

6: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB_Pepp:*

7: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB_Pepp:*

8: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Pepp:*

9: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB_Pepp:*

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18: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBCOMB_Pepp:*

19: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBCOMB_Pepp:*

19: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBCOMB_Pepp:*

10: /cgn2_6/ptodata/1/pubpaa/USIOD_PUBCOMB_Pepp:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-092-750-37
US-10-425-115-271834
US-10-037-417-1106
US-10-220-475A-4
US-10-419-629-4
US-10-072-012-448
US-10-696-699A-4
US-10-696-699A-4
US-10-425-114-71590
US-10-220-475A-17
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1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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US-10-220-475A-2
US-10-072-012-449
US-09-775-803-12
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          1566620 seqs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                         US-10-092-750-37
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                                                                                                                                                         Title:
Perfect score:
                                                                        ı
                                                                      protein
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                           Searched:
                                                                                                  Run on:
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No.
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Sequence 324612, Sequence 18, Appl Sequence 18, Appl Sequence 197766, Sequence 3714, App Sequence 78, Appl Sequence 3721, App Sequence 3721, App Sequence 3721, App Sequence 3722, App Sequence 24058, Sequence 270451, Sequence 270450, Sequence 270450, Sequence 21, Appl Sequence 51, A
                                     Sequence 279796,
Sequence 5116, Ap
Sequence 362182,
5 US-10-037-417-105
5 US-10-037-417-105
5 US-10-424-599-279796
7 US-10-425-115-362182
7 US-10-425-115-324612
4 US-10-308-846-18
5 US-10-220-475A-18
5 US-10-72-012-4776
6 US-10-72-012-124
7 US-10-77-701-36749
6 US-10-76-701-36749
7 US-10-76-701-36749
7 US-10-76-701-36749
7 US-10-76-701-36749
7 US-10-76-701-36749
7 US-10-78-701-361
7 US-10-78-701-361
7 US-10-425-115-24658
7 US-10-76-701-66525
7 US-10-76-701
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US-10-014-717-5
US-09-747-155-373
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US-09-771-730-41
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Gaps
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0
Sequence 37, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR PILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 176; DB 14;
100.0%; Pred. No. 2.8e-15;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTLOPRILONGOGHLPALPIWFLLOWLRLHPL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.
32; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-10-220-475A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-220-475A-4
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 271834
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION: DESCRIPTION: AUGLEW COURSELOW.
TITLE OF INVENTION: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                             Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179504C.1.pep
US-10-425-115-271834
                                                                                                                                                                                                                                                                                                                                                                                         37.2%; Score 65.5; DB 17;
48.4%; Pred. No. 4;
tive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 EQQQPHQPQLP-WFLQRQRPPVLLPWLRPHP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 QNQQQHLPALPIWF-----LLQWLRLHP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 106, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, David W
Padigaru, Muralidhara
Taupier Jr, Raymond J
Miller, Charles E
Eisen, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tcherney, Velizar T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iu, Xiaohong
pytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ellerman, Karen
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patturajan, Meera
Grosse, William M
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.4<sup>§</sup>
Matches 15; Conservative
                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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3 LOPR----LLQNQQQHLPALP---IWFLLQWLR 28
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                                                                                                                                                                                                                                                                                                                                                                                                      8 LSPROKEALAKFRENVODVLPALPNPDDYFLLRWLR 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 10/419,629
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE; CTHER INFORMATION: TAP-46 polypeptide
US-10-696-699A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71590, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative
SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 448 LENGTH: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-072-012-448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserva'
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NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taupier Colman, Steven D.

Gusev, Vladim..

Colman, Steven D.

Wolenc, Adam R.

F. Purtak, Katarzyna

(T: Grose, William M.

NT: Alsobrook II. John P.

ANT: Lepley, Denise M.

ANT: Lepley, Denise M.

ANT: Burges, Otherine E.

GOF INVENTION: Proteins and Nucleic Acids Encoding Same

E REFRENCE: 21402-228

ARBY FILING DATE: 2002-01-31

RICH APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-31

RICH APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR PLILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR PLILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-02-05

PRIOR PLILING DATE: 2001-02-05

PRIOR PLILING DATE: 2001-02-05

PRIOR PLILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR PLILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR PLILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,7459

PRIOR PLILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

"TADATE: 2001-02-07

"TADATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

"TADATE: 2001-02-07

"TADATE: 2001-02-07

"TADATE: 2001-02-08

"TADATE: 2001-02-09

"TADATE: 2001-
                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                    Query Match 32.4%; Score 57; DB 15; Length 403; Best Local Similarity 44.4%; Pred. No. 46; Matches 16; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LOPR-----LLQNQQHLPALP---IWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LSPROKEALAKFRENVÓDVLPALPNPDDYFLLRWLR 43
                                                                                                                                                                                            NAME/KEY: PEPTIDE
CTHER INFORMATION: TAP-46 polypeptide
US-10-419-629-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 448, Application US/10072012 Publication No. US20040033493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
      NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soreen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Oao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 71590
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10696699A

Publication No. US20040152883A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sanders, Bob G.
APPLICANT: Yu, Weiping
APPLICANT: Yu, Weiping
APPLICANT: Handah, Peras
TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof CURRENT APPLICATION NUMBER: US/10/696,699A
CURRENT APPLICATION NUMBER: US/10/696,699A
CURRENT APPLICATION NUMBER: 2003-10-29
DEFINE APPLICATION NUMBER: 2003-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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32.4%; Score 57; DB 15; Length 403; 44.4%; Pred. No. 46; 7; Indels 1:ive 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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Sequence 2, Application US/10220475A

Publication No. US2004002327A1

Publication No. US2004002327A1

APPLICANT: INFORMATION:

APPLICANT: ARAI, HIROYUKI

APPLICANT: NAN ENCODING

CURRENT APPLICANTION NUMBER: US/10/220,475A

PRIOR APPLICANTION NUMBER: PCT/JP01/01592

PRIOR APPLICANTION NUMBER: DC 200-57743

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver: 2.1

FENDING APPLICANTION OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VER: 21
TITLE OF INVENTION: Proceins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
FRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PLING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR PLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR PLICATION NUMBER: 60/265,412
PRIOR PLICATION NUMBER: 60/265,412
PRIOR PLICATION NUMBER: 60/265,395
PRIOR PLICATION NUMBER: 60/266,406
PRIOR PLICATION NUMBER: 60/266,767
PRIOR PLILING DATE: 2001-02-07
PRIOR PLICATION NUMBER: 60/267,459
PRIOR PLILING DATE: 2001-02-07
PRIOR PLILING DATE: 2001-02-07
PRIOR PRIOR APPLICATION NUMBER: 60/267,459
PRIOR PLILING DATE: 2001-02-07
PRIOR PLILING DATE: 2001-02-08
PREMAINING PLICAT Application data removed - See File Wrapper or PALM.
PROCEING APPLICATION VAINER: 60/267,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.1%; Score 56.5; DB 15; Length 400; Best Local Similarity 56.5%; Pred. No. 53; antiches 13; Conservative 3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 403;
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Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 QNQQQHLPALP---IWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 QNQQQHLPALP---IWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ENVODVLPALPNPDDYFLLRWLR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-072-012-451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-220-475A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-220-475A-2
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Sequence 17, Application US/10220475A

Publication No. US20040023227A1

SEQUENCE 17, MACTON:

APPLICANT: INOUE, KEIZO

APPLICANT: ARAIT, HIROYUKI

APPLICANT: ARAIT, HIROYUKI

APPLICANT: ARAIT, MAKOTO

CURRENT APPLICATION: DATE: 2002-08-30

CURRENT APPLICATION NUMBER: US/10/220,475A

CURRENT APPLICATION NUMBER: US/10/220,475A

PRIOR PILING DATE: 2001-03-01

PRIOR PILING DATE: 2000-03-02

PRIOR PILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE PATENTY OF THE PRIOR OF THE PRIOR PILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE PATENTY OF THE PRIOR OF THE PRIOR PILING DATE: 2000-03-02

SOFTWARE PATENTY OF THE PRIOR OF THE PRIOR PILING DATE: 2000-03-02

SOFTWARE PATENTY OF THE PRIOR OF THE PRIOR PILING DATE: 2000-03-02

SOFTWARE PATENTY OF THE PRIOR PATENTY OF THE PRIOR PILING DATE: 2000-03-02

SOFTWARE PATENTY OF THE PRIOR PATENTY OF THE PRIOR PILING DATE: 2000-03-02

SOFTWARE PATENTY OF THE PATENT
                                                                                                                                   Query Match 32.1%; Score 56.5; DB 15; Length 71; Best Local Similarity 32.5%; Pred. No. 9.9; Matches 13; Conservative 9; Mismatches 7; Indels 11
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                    ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17164H05_F11.pep
US-10-425-114-71590
                                                                                                                                                                                                                                                                                                4 OPRILONQOOHLPALPI-----WFLLOWL-----RLHPL 32
                                                                                                                                                                                                                                                                                                                                         Query Match 32.1%; Score 56.5; DB 15; Best Local Similarity 56.5%; Pred. No. 53; Matches 13; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 QNQQQHLPALP---IWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ENVÓDVĽPÁLPNPDDYFLLRWLR 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burgess, Catherine E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urtak, Katarzyna
kosse, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colman, Steven D.
Wolenc, Adam R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lepley, Denise M.
Rieger, Daniel K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-220-475A-17
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APPLICANT:
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APPLICANT:
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JOURNAL TO BE A PRICATION US/09775803
PUBLICATION NO. US2003016748741
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Remarktishnan, Vanitha
APPLICANT: Phillips, David
TITLE OF INVENTION: Transgenic Animals Having a Modified Glycoprotein V
TITLE OF INVENTION: Gene and Methods for Their Use
TITLE OF INVENTION: 124481-5044-US
CURRENT APPLICATION NUMBER: US/09/775,803
CURRENT FILING DATE: 1099-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
LENGTH: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.1%; Score 56.5; DB 10; Length 5
Best Local Similarity 46.7%; Pred. No. 74;
Matches 14; Conservative 2; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 105, Application US/10037417
Publication No. US20040052806A1
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Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Vernet, Corine A.M.
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Padigaru, Muralidhara
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APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiachong
APPLICANT: Spytek, Kimberly A
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Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
Shenoy, Suresh G
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Gorman, Linda
Edinger, Shlomit R
Sciore, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Mus musculus
US-09-775-803-12
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APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Guen, Stewen I.
APPLICANT: Gusev, Valdimir Y.
APPLICANT: Gusev, Valdimir Y.
APPLICANT: Gusev, Valdimir Y.
APPLICANT: Wolson, Adew R.
APPLICANT: Wolson, Milliam M.
APPLICANT: Grosse, Milliam M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Danise M.
APPLICANT: Rieger, Danise M.
APPLICANT: Rieger, Danise M.
APPLICANT: Burgese, Catherine E.
ITITE OF INVENTION: Proceins and Nucleic Acids Encoding Same CURRENT FILE OF INVENTION: Proceins and Nucleic Acids Encoding Same FILE REPRENCE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-31
PRIOR PLILOR DATE: 2001-01-31
PRIOR PLILOR DATE: 2001-01-31
PRIOR PLILOR DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266, 395
PRIOR APPLICATION NUMBER: 60/266, 767

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Best Local Similarity 56.5%; Pred. No. 53;
Matches 13; Conservative 3; Mismatches
                                                                                                   Sequence 449, Application US/10072012 Publication No. US20040033493A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                       Tchernev, Velizar
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
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US-10-072-012-449
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Gaps

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APPLICANT: Taupler Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Bisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                           CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
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Sequence 279796, Application US/10424599
| Publication No. US20040031072A1 |
| GENERAL INFORMATION: US20040031072A1 |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: Kovalic David K |
| APPLICANT: Kovalic David K |
| APPLICANT: Kovalic David K |
| APPLICANT: Cao Yongwei |
| TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TILLE OF INVENTION: Dayles and Uses Thereof for Plant Improvement |
| FILE REFERENCE: 38-21(5322)B |
| CURRENT PRILING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 285684 |
| SEQ ID NO 279796 |
| TYPE: RT |
| CORMINS : GIVENION |
| TYPE: RT |
| CORMINS : GIVENION |
| CORMINS : GIVENION
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US-10-424-599-279796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1%; Score 56.5; DB 15; Best Local Similarity 46.7%; Pred. No. 74; Matches 14; Conservative 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(90)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
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17 MKPRIVSLKIEHLVXLPRWFXTQVLK 42
PRIOR FILING DATE: 2001-02-28

PRIOR PLING DATE: 2001-03-02

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PRIOR APPLICATION NUMBER: 60/291,186

PRIOR PILING DATE: 2001-05-15

PRIOR PELING DATE: 2001-05-15

PRIOR PELING DATE: 2001-07-05

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NUMBER OF SEQ ID NOS: 227

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LENGTH: 567

TYPE: PRI

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US-10-037-417-105
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US-10-424-599-279796
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Search completed: November 11, 2004, 01:28:19 Job time : 35.4265 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
        Copyright
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OM protein - protein search, using sw model

November 10, 2004, 12:29:32; Search time 7.12953 Seconds (without alignments) 431.857 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-092-750-37 176 1 RTLQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	cal prot	hypothetical prote	_	hypothetical prote	ğ	ы	980	hglD protein - Ana	heterocyst glycoli	_	hypothetical prote		U	hypothetical prote	olfactory receptor	transporter, mfs s	hypothetical prote	hypothetical prote	hypothetical prote	escapes X-inactiva	cation-transportin	hypothetical prote	beta-galactosidase	eta-D-galactosid	H	N	22K zein precursor	zein	hypothetical prote
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38	48.5	27.6	790	N	AE2203		hypothetical prote
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C;Species:	: Caenc	Caenorhabditis elegans Oct-1000 #comience res	cis etc	gai	as Stricto	apredo +*e++	100 epac
C;Dare: 2	1-100-K	בכסות	adnemor		1 A T A T A D	CJUALE: ZY-OCC-1999 #Sequence_revision zy-Occ-1999 #CeAc_ch	
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A.Doforonce mumber: 701430	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		0000				
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A; Molecule type: DNA	e cype:	DINA CO.	:				
A;Residues: I-1360 <cou></cou>	8: I-I	360 400	^ 				
A;Cross-r	eferenc	ces: UN.	IPROT:(E 1	YK4; E	A, Cross-references: UNIPROT: Q9TYK4; EMBL: AF125461; PIDN: AAD12852.1;	12852.1; GSPDB:GNOUUZU; CESP:)
A;Experim	ental s	source:	straıı	66 C	ristol	L NZ; Clone Y8A9A	
C;Genetics:	: 0						
A; Gene: CESP: Y8A9A.2	ESP:Y82	49A.2					
A, Map position:	ition:	7					
A; Introns: 43/3;	: 43/3;		134/3	i,	74/1;	69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3;	87/3; 848/2; 944/2; 1044/2; 10
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אמרכוות			יאמרדאנ	n	'n	,	2430

hypothetical protein alr0717 [imported] - Nostoc sp. (strain PCC 7120)
hypothetical protein alr0717 [imported] - Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC1896
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DyA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Atle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AC1896
A;Accession: AC1896
A;Accession: AC1896
A;Accession: AC1806
A;Accession: 셤

3 LOPRILONQOOHLPALPIWFL-----LOWLRIHPL 32

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Length 225; 34.1%; Score 60; DB 2; Query Match

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R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odd
A;Reference number: A23701; MUID:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Buck, L.; Axel, R.
(edl 65, 175-187, 1991)
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for odc A;Reference number: A23701, MUD:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer, Nature 361, 353-356, 1993
Nature 361, 353-356, 1993
Aptille: Cloning and expression of odorant receptors.
A.Reference number: S29707; MUID:93149273; PMID:7678922
A.Accession: S29707.
                                                                                                                         A,Accession: H23701
A,Status: nucleid acid sequence not shown
A,Kotatus: nucleid mRNA
A,Residues: 1-314 <BUC>
A,Cross-references: UNIPAPOT:P23272; GB:M64388; NID:g205837; PIDN:AAA41751.1; PID:g205838
C,Superfamily: olfactory receptor OR14
C,Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:076054; GB:AL096881
C;Comment: This protein has the following properties: (i) alpha-tocopherol specific bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JC7708
R;Yamauchi, J.; Iwamoto, T.; Kida, S.; Masushige, S.; Yamada, K.; Esashi, T.
Biochem. Biophys. Res. Commun. 285, 295-299, 2018
Biochem. Biophys. Res. Commun. 285, 195-299, 2018
A;Title: Tocopherol-associated protein is a ligand-dependent transcriptional activator.
A;Reference number: JC7708; MUID:21338208; PMID:11444841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      olfactory receptor OR5 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: S29707; B37286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tocopherol associated protein - human
NyAlternate names: alpha-tocopherol associated protein
C.Species: Homo sapiens (man)
C.Spate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Residues: 193-236 <BUC>
A;Residues: 193-236 <BUC>
A;Cross-references: GB:M64375; NID:G205811; PIDN:AAA41738.1; PID:G205812
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.4%; Score 53.5; DB 2; Length 314; Best Local Similarity 40.7%; Pred. No. 11; Matches 11; Conservative 5; Mismatches 4; Indels
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A,Residues: 1-314 <RAM>
A,Cross-references: UNIPROT:Q04059
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A; Residues: 1-403 < YAM>
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A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T00333
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: Z14086; MUID:98290545; PMID:9628581
                                                                                                                                                                                                                                                                                               hypothetical protein VCA0173 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: F82493
                                                                                                                                                                                                                                                                                                                                                                                                                                             Riffeldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R., Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 466, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035, MUID:20406833; PMID:10952301
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A;Cross-references: UNIPROT:060306; EMBL:AB011132; NID:d1185402; PIDN:BAA25486.1
A;Experimental source: brain; clone HH1648
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C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: H23701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                     Gaps
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Pred. No. 31;
7; Mismatches 9; Indels
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                                     Indels
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A;Molecule type: mRNA
                                                                                              6 RLLQNQQQHLP-----ALPIWFLLQWLRLHPL 32
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Pred. No. 3.5;
0; Mismatches
   45.5%; Pred. No. 1.1; tive 3; Mismatches
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69.2%;
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Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 HLPALPIWFLLQW 26
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLPELPSWFPLAW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        olfactory receptor 19 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-162 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Accession: F82493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T00333
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A; Map position: 2

à g

A; Gene: VCA0173

A;Note: KIAA0560

RESULT 5

В 8

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosidues: 1.862 c PURA
A;Cross-references: UNIRROT:094441; EMBL:AL034583; PIDN:CAA22583.1; GSPDB:GN00066; SPDB:£
A;Experimental source: strain 972h-; cosmid c637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Status: preliminary; translated from GB/EWBL/DDBJ
A,Molecule type: DNA
A,Residues: 1.-240 cLNA
A,Residues: 1.-240 cLNA
A,Gross-references: UNIRROT:09Y7N1; EMBL:AL049559; PIDN:CAB40170.1; GSPDB:GN00068; SPDB::
A,Experimental source: strain 972h-; cosmid c1450
                                                     Cydcossion: B90558
Cydcossion: B90558
Cydcossion: B90558
RyChambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90558
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                   A.Residues: 1-292 <KUR>
A.Residues: 1-292 <KUR>
A.Cross-references: UNIPROT:Q98QJ1; GB:AL445566; PID:g14089784; PIDN:CAC13543.1; GSPDB:GRA;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40985
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21962
A;Accession: T40985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPAC637.04 - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
       Species: Mycoplasma pulmonis
Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T38996
R;Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL. Data Library, December 1998
A;Reference number: Z21823
A;Accession: T38996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 2;
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 2;
Pred. No. 47;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 LLKNSYEHPPSYPIKFLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LLQNQQQHLPALPIWFLLQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|:|:|
LEPKLIDNQYSLIPALP 83
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52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SPDB:SPCC1450.03
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SPDB:SPAC637.04
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A; Introns: 3/3; 41/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: MYPU 3700
A;Genetic code: SGC3
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AB2475

heterocyst glycolipid synthase [imported] - Nostoc sp. (strain PCC 7120)

Cypedies Nostoc sp. PCC 7120

A;Species Nostoc sp. PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AB2475

R;Kaneko, T: Nakamura, Y:, Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AB2475

A;Accession: AB2475
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C;Genetics:
A;Gene: hglD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
131334
hg1D protein - Anabaena sp. (fragment)
c;Species: Anabaena sp.
c;Species: Anabaena sp.
c;Species: Anabaena sp.
c;Date: 22-Ost-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
c;Date: 22-Ost-1399 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
c;Accession: T31334
A.Baceription: Heterocypt differentiation involves a new variant of polyketide or fatty
A.Reference number: Z21001
A.Recession: T3133
A.Accession: T3133
A.Accession: T3134
A.Accession: T313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q44221; EMBL:U13677; NID:9538374; PID:9538375; PIDN:AAA93154
C;Genetics:
A;Gene: hglD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B90558
hypothetical protein MYPU_3700 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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..
criptional activation involved in gene regulation in vivo in mammalian cells. C;Genetics:
A;Gene: tap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 448;
                                                                                                                                                            Length 403
                                                                                                                                                                                                                                     Indels
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illarity 54.5%; Pred. No. 21;
Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                      3 LOPR-----LLQNQQHLPALP---IWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                       8 LSPROKEALAKFRENVODVLPALPNPDDHFLLRWLR 43
                                                                                                                                                     Score 53; DB 2;
Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                                                                                                                                                         Query Match 30.1%;
Best Local Similarity 44.4%;
Matches 16; Conservative
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nes 12; Conservative
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Best Local Similarity
-heq 12; Conserve
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Search completed: November 10, 2004, 13:40:45 Job time : 8:12953 secs
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                                                                                                                                                                                             A;Residues: 1-314 <BUC>
A;Residues: 1-314 <BUC>
A;Cross-references: UNIPROT: P23274; GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: E75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: E75219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9V1Z4; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB4920
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               olfactory receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 22.Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S20571
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
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C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                            Gaps
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    DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lypothetical protein PAB2167 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.0%; Score 51; DB 2; Length 219; Best Local Similarity 31.8%; Pred. No. 16; Matches 7; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IWFLLOWLRL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%; Score 51.5; Dilarity 34.4%; Pred. No. 20; Conservative 7; Mismatches
29.3%; Score 51.5; D
ilarity 48.1%; Pred. No. 15;
Conservative 3; Mismatches
                                                                                                            50 RTLIPAMLINMQ---PSLAIW--LHWI 71
                                                                                1 RILOPRILIONOCOHLPALPIWFLLOWL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LLQNQQQHLPALPIWFLLQWLR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PRILIQNOQOHLPALP
  Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <KAW>
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A,Title: Expression of members of the putative olfactory receptor gene family in mammalia A,Reference number: $20571, MUID:92131132, PMID:1370859
A,Accession: $20571
                                                  A,Accession: S20571
A,Status: preliminary
A,Molecule type: DA
A,Molecule type: DA
A,Residues: 1-313 cPAR>
A,Residues: 1-313 cPAR>
A,Cross-references: UNIPROT:P30955, EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891
C,Superfamily: olfactory receptor OR14
C,Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                        Length 313;
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                                                                                                                                                                                                                                                     Score 51; DB
Pred. No. 23;
4; Mismatches
                                                                                                                                                                                                                                                        29.0%;
                                                                                                                                                                                                                                                                                                                                                           5 PRILONOCOHLPALP 19
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.34
Matches 8; Conservative
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norv norv norv

rattus 1 rattus 1

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Q99wwe rattus norv
P2372 rattus norv
P70526 rattus norv
Q8vgil mus musculu
Q8e906 shewanella
Q8e9154 pseudomonas
P88913 human herpe
P97871 mus musculu
Q15835 homo sapien
Q9apxi pseudomonas
Aat00534 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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38.1%; Score 67; DB 2; Length 1360;
Best Local Similarity 47.4%; Pred. No. 4.2;
Matches 18; Conservative 3; Mismatches 9; Indels
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Hypothetical protein.
SEQUENCE 1360 AA; 144313 MW; 312B206B6D087C3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Bristol N.A.
COurtnay (FIB-1995) to the EMBL/GenBank/DDBJ databases.
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STRAINEBLISTOOL N2;
Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1360 AA.
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                   090WW8
OLF9_RAT
P70526
Q8VG11
Q8E906
Q8HG48
Q8BJ54
P88913
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RK_HUMAN
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Q7N2F5
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, L
01-07-2003 (TrEMBLrel. 25, L
Hypothetical protein Y8A9A.2.
ORFNames=Y8A9A.2;
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  Caenorhabditis elegans.
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Submitted (NOV-2002)
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Q9TYK4
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    SOW SERVICE STREET STRE
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Qmaxz photcorhabdu
Q3408 coccyas er
O08742 mus musculu
Q95fs3 bradyrhizob
Q9b214 caiman croc
Q6pd61 homo saplen
Aah88915 homo saplen
Q86nx2 drosophila
Q86nx2 drosophila
Q76054 homo saplen
Cag30457 homo saplen
Cag30457 homo saplen
Q9213 rattus norv
Q615b2 homo saplen
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094zu3 mus musculu
072xB3 mus musculu
076x82 neurospora
074x42 giardia lam
095mz3 vibrio chol
08666 shewanella
060306 homo sapien
09udx3 homo sapien
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Aah69641 homo sapi
Q99ms0 rattus norv
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Q7r1b4 giardia lam
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                                                                                                                                        November 10, 2004, 12:27:34 ; Search time 39.0743 Seconds (without alignments) 471.205 Million cell updates/sec
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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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1 RILQPRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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09 WOM5915

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CAF05898
Q7QV42
Q9KMZ3
Q8EF60
060306
S144_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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Q7R1B4
Q8YYX5
Q7MZX2
Q7MZX2
Q9WZX086
G9V MOUSE
Q89FS3
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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SEQUENCE FROM N.A.
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O34086;
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Matches
                           RESULT 4
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KANEKO T., NAKAMURTA Y., WOLK C.P., KURILZ T., SASAMOCO S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
"Complete genomic sequence of the filamentous nitrogen-fixing
DNA Res. 8:205-213 (2001).

EMBL; APP03583; BAB72674.1; -.
PIR; AC1896; AC1896.
COMPLETE PROCEOME.
SEQUENCE 225 AA; 24777 MW; 96E6DFE80F9B66A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                         GLP 306 58193 60304.
Giardia lamblīa ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
35.2%; Score 62; DB 2; Length 703;
Best Local Similarity 56.0%; Pred. No. 9.9;
Matches 14; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%; Score 60; DB 2; Length 225; 45.5%; Pred. No. 5.4; ative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
1, AACB01000028; EAA41130.1; -.
JENCE 703 AA; 78310 MW; B7FF2CCE01F1810B CRC64;
417 LQPSLPQNQLRSLPALPLILLQPSLPLNQLRSLPAHPL 454
                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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                                                                                                                           703 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                           PRT;
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MEDLINE-21595285; PubMed=11759840;
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01-MAX-2002 (TrEMBLrel. 20,
01-NAR-2002 (TrEMBLrel. 20,
01-UIN-2003 (TrEMBLrel. 24,
Alr0717 protein.
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Best Local Similarity 45.5
Matches 15; Conservative
                                                                                                                         PRELIMINARY;
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NCBI_TaxID=103690;
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Q7R1B4;
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                                              Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Derose R., Derzelle S., Freysainet G., Gaudriault S., Redique C., Lanois A., Powell K., Siquier P., Vincent R., Wingate V., Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.; The genome sequence of the entomopathogenic bacterium Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=94356264; PubMed=8075835;

Avise J.C., Nelson W.S., Sibley C.G.;

"Why one-kilobase sequences from mitochondrial DNA fail to solve the Heatzin phylogenetic eniqua.";

Mol. Phylogenet. Evol. 3:175-184(1994).

-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
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Archosauria; Aves; Neognathae; Cuculiformes; Coccyzidae; Coccyzus.
                                                                                                                                                                                     Photorhabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Photorhabdus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64072 MW; CBEC7F62BF5E7852 CRC64;
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GO: GO: 001020; Chembrane; IEA.
GO: GO: 001020; E: electron transporter activity; IEA.
GO: GO: 0017004; P: cytochrome biogenesis; IEA.
GO: GO: 0018 p: electron transport; IEA.
InterPro; IPR003834; Ctytoch_TM.
InterPro; IPR006662; Thiored.
InterPro; IPR006663; Thiored.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Coccyzus erythropthalmus (Black-billed cuckoo)
575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Redox-active center.
SEQUENCE 575 AA; 64072 MW; CBEC7F62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luminescens.";
Nat. Biotechnol. 21:1307-1313(2003).
EMBL: BX571872; CAE16511.1; -.
PhotoList; plu4139; -.
PRT;
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MEDLINE=22957627; PubMed=14528314;
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PROSITE; PS00194; THIOREDOXIN; 1.
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Pfam; PF00085; Thioredoxin; 2.
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les 10; Conservative
PRELIMINARY;
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Q89FS3
    OCC CONTRACT LANGE BETT LANGE BET
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STRAIN-C57BL/6; TISSUB-Liver;
STRAIN-C57BL/6; TISSUB-Liver;
MEDLINE-97275136; PubMed=9129030;
Ravanat C., Morales M., Azorsa D.O., Moog S., Schuhler S., Grunert P.,
Loew D., van Dorsselaer A., Cazenave J.-P., Lanza F.;
"Gene cloning of rat and mouse platelet glycoprotein V: identification of megakaryocyte-specific promoters and demonstration of functional
complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin cleavage.";
Blood 89:3253-3262(1997).
-!- FUNCTION: The GPID-V-IX complex functions as the von Willebrand factor receptor and mediates von Willebrand factor-dependent platelet adhesion to blood vessels. The adhesion of platelets to injured vascular surfaces in the arterial circulation is a critical initiating event in hemostasis (By similarity).
-!- SUBCELULLAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                      -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                   Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 320 3516 MW; B277E235154D235A CRC64;
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8
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05-JUL-2004 (Rel. 44, Last annotation update)
Platelet glycoprotein V precursor (GPV) (CD42D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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15-JUL-1998 (Rel. 36, Last seq
05-JUL-2004 (Rel. 44, Last anno
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31.0%;
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008742;
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NON TER
SEQUENCE
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GPV MOUSE
DD 08748
DT 15-JUL
DT 15-JU
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EMEL; Z69595; CAA93441.1; -.

R HSEP; QBEZE6; 102N.

R MGD; MGI: 1096365; GPS.

R InterPro; IPRO01611; LRR_Cterm.

R InterPro; IPRO03591; LRR_Cterm.

R InterPro; IPRO03591; LRR_CYP.

R Ffam; PF01660; LRR; 13.

R Ffam; PR00560; LRR; 13.

R FAMT; SM00362; LRRCT; 1.

R SWART; SM00362; LRRCT; 1.

R MART; SM00362; LRRCT; 1.

R MART; SM00362; LRR_TYP; 10.

R MART; Robeat; Signal; Treamembrane.

R DOAD TO TO THE TYP; 10.

R DIOA Coagulation; Cell adhesion; Glycoprotein; Leucine-rich repeat;

R JICAL TO TO THE TYP; 10.

R DOAD TO THE TY
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 57.5;
46.7%; Pred. No. 32
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N-linked
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385
567 AA;
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B116626 protein.
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CARBOHYD
CARBOHYD
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16; Conservative
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      sapiens (Human)
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Anke A., Expendeck D., Milsson M., Arnason U.;

Anke A., Expendeck D., Milsson M., Arnason U.;

The mitochondrial genomes of the iguana (Iguana iguana) and the cained (Cained Cained Cai
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Archosauria, Crocodylidae, Alligatorinae, Caiman.
                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                              Ouery Match
32.4%; Score 57; DB 2; Length 111;
Best Local Similarity 39.3%; Pred. No. 6.5;
Matches 11; Conservative 6; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
                                                                                                                                      111 AA; 12601 MW; E2F95EF338B88AB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion, NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 352 AA; 38810 MW; 68197AA6DD36D8A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     5 PRLLQNQQQHLPALPIWFLLQWLRLHPL 32
                                                                                                                                                                                                                                                                                                                                                                           5 PRLLQNQQQHLPALPIWFLLQWLRLHPL 32
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InterPro; IPR010933; NaDH_deby_S2_C.
InterPro; IPR0110933; NaDH_deby_S2_C.
Pfam; PF06444; NaDH_deby_S2_C; 1.
Pfam; PF00361; Oxidored_q1, 1.
Bradyzhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL, AP005559; BAC51891.1; -.
CCMplete proteome.
SEQUENCE 111 AA; 12601 MW; E2F95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21190842; PubMed=11297180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Q6PD61;
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Willing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Antiring M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Arzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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Mammalia; Eutheria, Primata, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 392 AA, 44747 MW; 11A833345968FE5A CRC64;
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ID AAH88915

AAH88915

D AAH88915

DT 02-WAR-2004 (TrEMBLrel. 27, Created)

DT 02-WAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-WAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-WAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Charyota, Meaazoa, Chordata, Craniata, Vertebrata; Eutocommania, Eutheria, Primata; Catarrhini, Hominidae; Hom NCB TaxxD=9606,

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RX MEDLINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
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EMBL, BCOS8915, AAH58915.1;

InterPro; IPRO01251; CRAL TRIO C.

InterPro; IPRO01071; RetBInd/toCTrans.

InterPro; IPRO01071; RetBInd/toCTrans.

InterPro; IPRO08983; TNP like N.

Pfam; PF00565; CRAL TRIO, 1.

Pfam; PF00565; CRAL TRIO, 1.

PRINTS; PR00169; CRAL TRIO, 1.

PRINTS; RN00516; SEC14; 1.

PROSTE; PS050161; CRAL TRIO, 1.
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Ketchum K.A.,

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Jalali
Kimmel
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                 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
Brownstein M.J., Ubdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Anilalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rack S.A., McLan M., Sodergren E.J., Lu X., Gibbs R.A.,
Rack S.A., Morley K.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
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Andriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schwutz J., Myers R.M., Bouffard G.G.,
Generation and initial analysis of more than 15,000 full-length human
T. Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16993(2002).
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MEDINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Holt R.M., Hoskins R.A., Galle R.F.,

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Barton G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Ffeiffer B.D.,

Amil J.F., Agbayani A., An H.J., Andrews-Ffannkor G.E.,

Anti J.F., Agbayani A., An H.J., Andrews-Ffannkor G.L.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Barkova D., Botchan M.R., Bouck J., Broketeir P., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Cholson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Burtis K.J., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Hennan T.J., Wei M.H., Ibegwam C.,

Hottin D., Houston K.A., Henland T.J., Wei M.H., Ibegwam C.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteryera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 32.4%; Score 57; DB 2; Length 392; Local Similarity 44.4%; Pred. No. 25; near 16; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
TISSUE=Erain;
Strausberg H. S. Strausberg (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058915; AH58915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 392 AA; 44747 MW; 11A833345968FE5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=CG13902;
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Matches
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Kimmel B.E., Kodira C.D., Karatiz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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Millams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
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MEDLINE=2242606; PubMed=12537568;
MEDLINE=2242606; PubMed=12537568;
Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patels D.J.M., Patk S., Sedergren E.J., Richards S., Sodergren E.J., Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., melanogaster euchromatic genome sequence.", George Biol. 3:RESBARCH0079-RESBARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: systematic review."; Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003469; AAF47420.1; -.
Flyamase; FBGT003166; CG133902.
InterPro; IPR007113; Cupin region.
InterPro; IPR003347; TF_JmJC.
Pfam; PF02373; JmJC; 1.
SEQUENCE 394 AA; 44323 MW; 03E15F55F25EF503 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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nilarity 54.2%;
Conservative 1
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q86NX2; Q86NX2

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RESULT 12
086NXZ
AC 086NX
AC 086NX
DT 01-JU
DT 0

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REWEIGHERON N.A.

SEQUENCE FROM N.A.

REDIGERIES DEMONDED TO 10101038/990031;

RAY REDIGERS PURMED TO S. BTUSKEWACH R. Beare D.M.,

DUNDAM I. HURT A.R., AINSCOUNT R., Almeida J.P., Bebased A.K.,

RAG Clamp, M. Smink L.J., AINSCOUNT R.A. Almeida J.P., Bebased A.K.,

RAG CLAMP, D. SELEN B. BERICOW R.F., BATES K.N. BERSEN S. B.

BING C.P., Blakey S.B., Bridgeman A.M. BUCK D. BURGES J.,

RAG CORNOY D. CODPY V. COLOGO C.C. COLLIET R.E., CONDON R. COLOGO V. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain."; DNA Res. 6:329-336(1999).
-!- FUNCTION: Carrier protein. Binds to some hydrophobic molecules and
                                                                                                                           TISSUE-Liver;
PubMed=1122624; DOI=10.1073/pnas.041620398;
Shibata N., Arai M., Misaki Y., Dohmae N., Takio K., Ono T.,
Inoue K., Arai H.;
"Supernatant protein factor, which stimulates the conversion of squalene to lanosterol, is a cytosolic squalene transfer protein and enhances cholesterol biosynthesis.";
Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249(2001).
Tocopherol-associated protein is a ligand-dependent transcriptional
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Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
Collins J.E., Huckle E.J.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION
                               ctivator.";
iochem. Biophys. Res. Commun. 285:295-299(2001).
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                                    activator.
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076054; OPULN4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP)
(HTAP) (Supernatant protein factor) (SPF) (Squalene transfer protein).
Homo sapiens (Human).
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MEDLINE-21338208; PubMed=11444841; DOI=10.1006/bbrc.2001.5162;
Manauchi J., Iwamoto T., Kida S., Masushige S., Yamada K., Esashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A novel human tocopherol-associated protein: cloning, in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidaa; Drosophilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.4%; Score 57; DB 2; Length 401; 54.2%; Pred. No. 26; Live 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), ALTERNATIVE SPLICING, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                  401 AA.
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J. Biol. Chem. 275:25672-25680(2000).
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                                                    176 OPTLILNTIOHWPALHKWLDLNYL 199
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          27
                                                                                                                                                                                                                                     Created)
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FlyBase, FBgn0035166, CG13902.
InterPro; IPR007113; Cupin region.
InterPro; IPR00347; TF_JmJC.
Pfam; PF02373; JmjC; 1.
SMART; SM00558; JmjC; 1.
          OPRLIONOCOHLPALPIWFLEOWL
                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   ORFNames=CG13902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              GM21055p.
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Query Match

Matches

S142_HUMAN

28

3 LOPR----LLQNQQQHLPALP---IWFLLQWLR

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DR GO; GO:0005549; C:cytoplasm; NAS.

DR GO; GO:0005549; C:cutleus; NAS.

DR GO; GO:0005549; C:cutleus; NAS.

DR GO; GO:0005549; F:phospholipid binding; NAS.

DR GO; GO:0005549; F:phospholipid binding; NAS.

DR GO; GO:00045893; F:phospholipid binding; NAS.

DR GO; GO:00045893; F:phospholipid binding; NAS.

DR GO; GO:0045893; P:positive regulation of transcription, DNA-d.

DR GO; GO:0045893; P:positive regulation of transcription, DNA-d.

DR GO; GO:0045893; P:positive regulation of transcription, DNA-d.

DR GO; GO:0045893; P:positive regulation of the control biosynthesis; NAS.

DR InterPro; IPR00121; CRAL_TRIO_N.

DR InterPro; IPR00101; RetBind/tooTrans.

DR InterPro; IPR00101; RetBind/tooTrans.

DR InterPro; IPR001001; RetBind/tooTrans.

DR Fam; PF00560; CRAL_TRIO_N; 1.

DR PRINTS; PR006160; CRAL_TRIO_N; 1.

DR PRNSTT; PR006160; CRAL_TRIO, 1.

DR PROSITE; PS0066; GOLD; 1.

DR PROSITE; PS0066; GOLD; 1.

KW 3D-structure; Activator; Alternative splicing; Lipid-binding;

KW Nuclear protein; Transcription regulation; Transport.

DR PADAL

TRIO CRAL_TRIO.

TO CRAL_TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
promotes their transfer between the different cellular sites.

Binds with high affinity to alpha-tocopherol. Also binds with a weaker affinity to other tocopherols and to tocotrienols. May have a transcriptional activatory activity via its association with alpha-tocopherol. Probably recognizes and binds some squalene structure, suggesting that it may regulate cholesterol biosynthesis by increasing the transfer of squalene to a metabolic subdivity monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol.
                                                                                                                                                                                                                                                                                                                                                                                                                    Name=3;
IsoId=076054-3; Sequence=Not described;
TISSUE SPECIFICITY: Widely expressed. Strong expression in liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.4%; Score 57; DB 1; Length 403; 44.4%; Pred. No. 26; 7; Indels iive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain and prostate.
-!- DEVELOPMENTAL STAGE: Low expression in fetal tissues.
-!- SIMILARITY: Contains 1 CRAL-TRIO domain.
-!- SIMILARITY: Contains 1 GOLD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 2).
/FTId=VSP 006031.
Y -> H (in Ref. 2).
D846747EC8D1513E CRC64;
                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                          Name=2;
IsoId=076054-2; Sequence=VSP_006031;
                                                                                                                                                                                                                                                                                                                                                    IsoId=076054-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL096881; CAB51405.1; -. EMBL, AC04832; AAF19256.1; -. ERNBL, BAA86500.1; -. PIR, JC7708; JC7708. PDB; 106U; X-ray; A/C/E=1-403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOGU; X-ray; A/C/E=1-403.
HGNC:10699; SEC14L2.
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403 AA; 46145 MW;
                                                                                                                                                                                                                                                                                                                                Name=1;
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Gaps

10;

Conservative

Best Local Similarity Matches 16; Conserv

Query Match

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AZIA. A. M. A CONTROLL OF CONTROL OF CONTROL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A,
Coll C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E
Beare D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR456571; CAG30457.1;
SEQUENCE 403 AA; 46145 MW; D846747EC8D1513E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP)
(bTAP) (Fragment).
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MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.
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                                                                                                                                                                                                                             CAG30457;
01-UTN-2004 (TrEMBLrel. 27, Created)
01-UTN-2004 (TrEMBLrel. 27, Last sequence update)
01-UTN-2004 (TrEMBLrel. 27, Last annotation update)
SEC1412 protein.
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TISSUE=Liver;
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NCBI_TaxID=9913;
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P58875;
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S142 BOVIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are to restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
structure, suggesting that it may regulate cholesterol
blosynthesis by increasing the transfer of squalene to a metabolic
active pool in the cell (By similarity).
-!- SUBGNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol, and nuclear in presence of alpha-tocopherol (By similarity).
-!- SIMILARITY: Contains 1 GOLD domain.
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3; Mismatches
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Matches 13; Conservative
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Search completed: November 10, 2004, 13:38:39 Job time : 41.0743 secs

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Sequence 14886, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 38576, A
Sequence 14171, A
Sequence 14171, A
Sequence 18690, A
Sequence 48396, A
Sequence 48396, A
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19500, A
61329, A
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45804, A
18106, A
13147, A
2, Appli
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Sequence 15547, A
Sequence 27928, A
                                                                               November 10, 2004, 12:32:37; Search time 12.7807 Seconds (without alignments) 191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-248-796A-15547

US-09-248-796A-15547

US-09-217-12

US-08-217-12

US-08-217-12

US-08-212-188-2

US-08-970-725-2

US-08-970-725-2

US-09-270-76-385-6

US-09-270-76-385-6

US-09-270-76-38178

US-09-270-76-48395

US-09-288-796A-14171

US-09-288-796A-14171

US-09-288-796A-14171

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US-09-288-796A-18928

US-09-288-796A-18928

US-09-538-092-1171

US-09-538-092-1171

US-09-538-092-1171

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US-09-548-796A-18106

US-09-270-767-61329

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US-08-455-543A-55
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Maximum Match 100%
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56, Appl	56, Appl	54, Appl	54, Appl	25, Appl		52, Appl		4, Appli	4, Appli	17, Appl	53, Appl	53, Appl	60, Appl	2963, Ap	19923, A	2, Appli	370, App
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US-08-455-543A-56	US-08-223-305C-56	US-08-455-543A-54	US-08-223-305C-54	US-07-745-206A-25	US-08-455-543A-52	US-08-223-305C-52	US-08-311-363-25	US-08-713-118-4	US-09-452-007-4	US-10-162-012-17	US-08:455-543A-53	US-08-223-305C-53	US-09-556-818-60	US-09-583-110-2963	US-09-248-796A-19923	US-09-435-376-2	US-08-905-223-370
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28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Sequence 15547, Application US/09248796A
Sequence 15547, Application US/09248796A
Patent No. 6747137
Faceback INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANC
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
RRICR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15547
                                                                            GENERAL INCORNATION:

APPLICANT: Lynn Doucette-Stamm et al.

APPLICANT: Lynn Doucette-Stamm et al.

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

CURRENT PAPLICATION NUMBER: US 09/107,433

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR PLING DATE: 1998-06-30

PRIOR PLING DATE: 1998-06-12

PRIOR PLING DATE: 1998-06-12

PRIOR PLING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 53.22

SEQ ID NO 44.33
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Best Local Similarity
Matches 11; Conserv
US-09-583-110-4473
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock ad al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: 08/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

SEQ ID NOS: 28208

SEQ ID NO 14886

LENGTH: 750
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Pred. No. 38;
3; Mismatches 18; Indels
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Sequence 2, Application US/08212188

Patent No. 5689039

GENERAL INFORMATION:
APPLICANT: BECKER, JEFFREY M.
APPLICANT: STACEY, GARY
TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: HOWREY & SIMON
STREET: 1299 PERNSYLVANIA AVE., N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,188
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ATTORNEY/AGENT INFORMATION:
NAME: AUGRBACH, JEFRREY I RECISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 7493-006
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 383-7451
                            551 IGLTIHESTNKDEVGPLKKKINGTVL 576
1 MAVIINELSQRDSCGPLKISLNNKIL 26
                                                                                                                                                                   Sequence 14886, Application US/09248796A; Patent No. 6747137
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Best Local Similarity 39.0%;
Matches 16; Conservative 3
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TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2
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LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                              US-09-248-796A-14886
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J Sequence 27928, Application US/09248796A

J TILLE OF INVENTION: NUMBER: US/09/248,796A

J CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

J WUMBER OF SEQ ID NOS: 28208

LENGTH: 95
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PB461PPT:
CURRENT FILING DATE: 2001-04-24
CURRENT FILING DATE: 2001-04-24
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,296
PRIOR PILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-05-07
STORYMARE: PALENT DATE: 1998-05-07
SOFTWARE: PALENT DATE: 2001-07
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                                                                                                                   DB 4; Length 904;
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                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 ITHKASCKDLSVSSRNKLLAPLIMTDTVGLIFLDFTP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LSQRDSCGPLKISLNNKIL------VYGNLFSSFTP 37
                                                                                                                   Query Match 28.3%; Score 53; DB Best Local Similarity 41.7%; Pred. No. 16; Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11arity 34.6%; Pred. No. 34; Conservative 7; Mismatches
                                                                                                                                                                                                                                                    12 DSCGPLKISLNNKILVYGNLFSSF 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09830217
Patent No. 6521441
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                  TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-15547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 12
LENGTH: 691
LENGTH: 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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RESULT 9
US-09-270-767-38576

JOS-09-270-767-38576

Sequence 38576, Application US/09270767

Sequence 38576, Application US/09270767

Patent No. 6703491

GRENEAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

FILE REPERENCE: File Reference: 7326-094

CURRENT PELING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 38576

LENGTH: 160

LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49, DB 5; Length 610;
Pred. No. 42;
9; Mismatches 12; Indels
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25.7%; Score 48; DB 4; Length 160;
Best Local Similarity 33.3%; Pred. No. 10;
Matches 12; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTER: IBM PC compatible
CORPTARE: Barentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02708
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 7493-006
TELECOMMUNICATION INFORMATION:
                                                                           PLANT PEPTIDE TRANSPORT GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LSQRDSCGPLKISLN----NKIL----VYGNLFSSF 35
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                                                                                                                                                                     SEEE: HOWREY & SIMON
1: 1299 PENNSYLVANIA AVE., N.W.
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Arabidopsis thalliana
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 610 amino acids
amino acid
      APPLICANT: BECKER, JEFFRE APPLICANT: STACEY, GARY TITLE OF INVENTION: PLANT NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE: ATPTR2AP
PCT-US95-02708-2
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                                                                                                                                                                                                                                                               Score 49; DB 1; Length 610
Pred. No. 42;
9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2. Application US/08970725
Patent No. 6080542
CENERAL INFORMATION:
APPLICANT: Becker, Jeffrey M.
TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,725
FILING DATE: 14-NOV-1997
CLASSIFICATION NUMBER: US 08/212,188
ATTORNEY/AGENT INFORMATION:
NAME: WEIGHT I
                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : : | | : : | | : 36 INQADEQSSTDELQKSMSTGVLVNGDLYPSPT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 INQADEQSSTDELQKSMSTGVLVNGDLYPSFT 67
                                                                                                                                                                                                                                                                                                                                                                                                  5 INELSQRDSCGPLKISLNNKILVYGNLFSSFT 36
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thalliana
IMMEDIATE SOURCE:
CLONE: ATPTR2AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
PCT-US95-02708-2
PCT-GS95-02708-2
, Sequence 2, Application PC/TUS9502708
, GENERAL INFORMATION:
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TELEPHONE: 215-875-8383
TELEPHONE: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               26.2%;
34.4%;
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 34.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 11; Conserv
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STATE: PA
COUNTRY:
                                                                                                                                                                  ; CLONE: 7
US-08-212-188-2
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RESULT 14
US-09-270-767-48395
is Sequence 48395, Application US/09270767
j Patent No. 6703491
j GENERAL INFORMATION:
i APPLICANT: Homburger et al.
j TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
j TITLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
j CURRENT FILING DATE: 1999-03-17
j CURRENT ELING DATE: 1999-03-17
j SOFTWARE: PatentIn Ver. 2.0
j SEQ ID NO 48395
i LENGTH: 151
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US-002-270-767-33178
US-002-270-767-31178
Sequence 33178, Application US/09270767
Sequence 33178, Application US/09270767
Sequence 3118, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33178
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                              Query Match 25.7%; Score 48; DB 4; Length 414; Best Local Similarity 32.1%; Pred. No. 36; Matches 9; Conservative 7; Mismatches 12; Indels
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Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47.5; D
Pred. No. 11;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Xaa means any amino acid US-09-270-767-48395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      :|:::::| || || : |:
145 LALVLEDLFPRDGLGPLHAELGRAMHVF 172
                                                                                                                                                                                                                                                                                                                                                                     1 MAVIINELSQRDSCGPLKISLNNKILVY 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RDSC----GPLKISLNNKILVYG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 RDSCQGDSGGPLVTSIDGQLKLYG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RDSC----GPLKISLNNKILVYG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18690
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 41.7%;
Matches 10; Conservative
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US-09-248-796A-14171

Sequence 14171, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICAMY: Keth Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14171
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 53793

LENGTH: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 25.7%; Score 48; DB 4; Length 160; Similarity 33.3%; Pred. No. 10; 12; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VSMADNCGNLRLSMNELSGNEYLPSANAYGMQYEDF 38
        3 VSMADNCGNLRLSMNELSGNEYLPSANAYGMQYEDF 38
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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, Patent No. 6551795
, GENERAL INFORMATION:
                                                                                RESULT 10
US-09-270-767-53793
Sequence 53793, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 11; Conserv
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Matches 12; Conserv
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71 RDSCQGDSGGPLVTSIDGQLKLYG 94

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us-10-092-750-38.rai
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RESULT 15

US-09-248-796A-14928

JSequence 14928, Application US/09248796A

Sequence 14928, Application US/09248796A

PAPELICANT: Reith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/0948, 796A

CURRENT FILING DATE: 1999-02-13

FRIOR APPLICATION NUMBER: US 60/096, 409

FRIOR PILING DATE: 1998-08-13

FRIOR PILING DATE: 1998-08-13

FRIOR FILING DATE: 1998-08-13
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RESULT 1
US-10-092-750-38
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Sequence 5855, Ap
Sequence 10198, Ap
Sequence 4173, Ap
Sequence 311744,
Sequence 267293,
Sequence 55925, A
Sequence 18964,
Sequence 280511,
Sequence 280511,
                                                                                                                     November 10, 2004, 16:36:12; Search time 39.7478 Seconds (without alignments) 328.807 Million cell updates/sec
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1. 'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. 'cgn2_6/ptodata/1/pubpaa/DTO7_NEW_PUB_pep:*
3. 'cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
4. 'cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5. 'cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7. 'cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
20. 'cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                            1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 15 US-10-282-122A-78432

1 4 US-10-369-493-5855

1 4 US-10-369-493-5855

1 9 US-09-738-626-4773

2 17 US-10-425-115-267293

1 15 US-10-425-115-31744

1 15 US-10-425-115-31741

1 15 US-10-425-114-64080

1 15 US-10-425-115-18664

6 17 US-10-425-115-18664

6 17 US-10-425-115-18664

6 17 US-10-425-115-18664

6 17 US-10-437-963-126350
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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187
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Match Length DB
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Sequence Sequence	5223,	Sequence 3 Sequence	Sequence	8 Sequence	Sequence	s Sequence	Sequence	Sequence	6 Sequence 161016	Sequence 103	9	78	Sequence	Sequence 22	l Sequence 197	7 Sequence 183	133	133	Sequence 35254	3649,	equence 56, Ay	equence 30538	Sequence 53217,	38,	Sequence Sequence	04 Seguence 1435	85 Seguence 1435	53 Sequence 1708
US-10-437-963-1193 US-10-282-122A-531	US-09-815-242	US-10-278-946-1 US-10-282-122A-	US-10-424-599-2218	US-10-437-963-1310	US-10-437-963-1797	US-10-437-963-15	US-10-424-599-1736	US-10-437-963-1586	US-10-437-963-1610	US-10-292-798-1024	US-10-437-963-1955	US-10-252-734-7	US-10-252-734-79	US-10-424-599-22	US-10-424-599-1	US-10-424-599-18	US-09-860-670-13	US-10-227-646-13	US-10-767-701-3525	US-10-108-260A-364	US-10-786-720-56	US-10-425-115-3053	US-10-425-114-5321	US-10-166-087-3	425-115-2888	US-10-437-963-1435	US-10-437-963-1435	US-10-424-599-1708
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114	15	8 6	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	4	45

ALIGNMENTS

. 0 Query Match
100.0%; Score 187; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 37; Conservative 0; Mismatches 0; Indels Sequence 38, Application US/10092750
; Sequence 38, Application US/10092750
; Publication No. US20030032157A1
GENERAL INFORMATION:
 APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
APPLICANT: Mright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE PREFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US 60/274,526
; RIOR PLING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FRRESEQ for Windows Version 4.0
; LENGTH: 37 TYPE: PRT
CORGANISM: Homo sapiens
US-10-092-750-38

. 0

Gaps

RESULT 2
US-10-282-122A-78432
; Sequence 79432, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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Sequence 10198, Application US/10369493
; Sequence 10198, Application US/10369493
; Publication No. US20030233675A1
GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Glater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; FILE OF INVENTION NUMBER: US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360, 039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10198
LENGTH: 324
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Pred. No. 24;
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                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                 4; Mismatches
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HANDO, SEIKO
APPLICANT: OCHIAI, MEIKO
APPLICANT: OCHIAI, MEIKO
APPLICANT: OCHIAI, MENIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TENDA, MASATO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: OZAKI, AKO
ITILE OF INVENTON: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2000-12-18
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                238 GEYSVSVDGKSLYYGNMMSDVTP 260
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PRIOR FLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                    15 GPLKISLNNKILVYGNLFSSFTP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4773, Application US/09738626
Publication No. US20020197605A1
                                     ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10198
                                                                                                                                                                           Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-10-369-493-10198
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LENGTH: 619
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; Sequence 5855, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Gladman, Barry S.
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION NUMBER: US 60/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-09

PRIOR PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PRIOR DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-20

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001
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                                                                                                    Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                                                                                                                               Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 50.04
Matches 13; Conservative
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ORGANISM: Yersinia pestis
US-10-282-122A-78432
                                                                                                                                                                                                                                                 Trawick, John
                                 Zamudio, Čarl
Malone, Chery
   Wang, Liangsu
                                                                                                                                                                                                            Wall, Daniel
                                                                                                                                                                              Zyskind,
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Seeven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Paparka, Jack E
APPLICANT: Paparka, Jack E
APPLICANT: Paparka, Jack E
APPLICANT: Paparka, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
FORMEN FILING DATE: 2003-04-28
FEATURE: PRI
APPLICANT: Associated With
A
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Publication No. US20040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Young
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 311741
LENGTH: 437
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               Gaps
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       7;
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           Indels
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US-10-425-114-65925
                                                                                                                                 28 LVVGTTSLAQSSSLGPLRISPWNK-----STSFTP 57
           11;
                                                                               1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
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US-10-425-115-311741
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; Sequence 65925, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
               4.
           15; Conservative
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ORGANISM: Zea mays
FEATURE:
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               Matches
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US-10-425-115-267293
US-10-425-115-267293
Sequence 267293, Application US/10425115
Sequence 267293, Application US/10425115
Sequence 267293, Application No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Numbers US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 267293
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 311744, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 311744
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                                                                                                                                                                                                                                                          Query Match
27.8%; Score 52; DB 9; Length 755;
Best Local Similarity 35.3%; Pred. No. 88;
Matches 12; Conservative 5; Mismatches 17; Indels
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US-10-425-115-267293
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US-10-425-115-311744
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TYPE: PRT
TOGANISM: Corynebacterium glutamicum US-09-738-626-4773
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4773
LENGTH: 755
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Best Local Similarity
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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       Sequence 64080, Application US/10425114

Sequence 64080, Application US/20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Avoil C. David K.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Tabaska, Jack E.

APPLICANT: TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPREMENCE: 38-21(5313)8

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 441
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalio, David K.
APPLICANT: Kovalio, David K.
APPLICANT: Calou, Yihua
APPLICANT: Calou, Yihua
APPLICANT: Calou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 198064
LENGTH: 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
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US-10-425-114-64080
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; OTHER INFORMATION: Clone ID: MRT4577_112213C.1.pep
MCs-10-425-115-198064
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27.5%; Score 51.5; D:
Best Local Similarity 34.4%; Pred. No. 54;
Matches 11; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 198064, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
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US-10-425-115-198064
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US-10-425-114-64080
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Sequence 126350, Application US/10437963
; Sequence 126350, Application US/10437963
; Sequence 126350, Application US/10437963
; Publication No. US20440123343a1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Branch Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(23221) B
; CURRENT APPLICATION NUMBER: 2003-05-14
; CURRENT FILING DATE: 2003-05-14
; CURRENT FILING DATE: 2003-05-14
...crilCANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 280511
LECTH: 66
TYPR: n=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_95323C.1.pep
US-10-424-599-280511
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US-10-437-963-126350
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26.7%; Score 50; DB 16;
Best Local Similarity 30.8%; Pred. No. 31;
Matches 12; Conservative 8; Mismatches 17.
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Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wai
APPLICANT: Wu, Wai
APPLICANT: Wu, Wai
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-10-437-963-119330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-437-963-126350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 126350
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:29:32; Search time 8.24352 Seconds (without alignments) 431.857 Million cell updates/sec

Title: US-10-092-750-38
Perfect score: 187
Sequence: 1 MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	polyprotein - infe	probable exported	a]	hypothetical prote	a]	hypothetical prote	probable TonB-depe	TonB-dependent rec	conserved hypothet	hypothetical prote	hypothetical prote	related to spore c	cell surface prote	hypothetical prote	ċ	ĕ	a)	core antigen - hep		Ω.	hypothetical prote	general secretion	å	N	twitchin [similari	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
SUMMARIES	DI	T00327	AH0446	~	H90538	H84862	875372		D81215	B98021	G90091	E90284		T17456		G89935	S16748		S53221				0	4156	8885	572	2793	~	T20609	S59384
	DB	0	~	7	N	N	~	~	~	7	~	7	N	N	N	~	N	N	N	N	N	N	N	7	N	(7)	7	~	~	7
	Length	ı co	30		1128	0	m	0	0	0	7	4,	φ	0	S)	QJ.	4	S	183	2	N	œ	н	m	83	m	16	-	79	ന
æ	Query Match		0	a	29.1	œ	æ	æ	æ	æ	œ	7	~	~	ø	9	ø	Φ	φ	φ	9	S	S	S	S	S	2	S	ß	S
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Gaps

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Query Match 30.5%; Score 57; DB 2; Length 1307; Best Local Similarity 50.0%; Pred. No. 11; Matches 13; Conservative 3; Mismatches 10; Indels

hypothetical prote	ADP-ribosyl cyclas	chalcone synthase	hypothetical prote	hypothetical prote	ribulose-bisphosph	ribulose-bisphosph	genome polyprotein	hypothetical prote	hypothetical prote	MHC class II OLA-D	hypothetical prote	glutamate-5-semial	gamma-glutamylphos	gamma-glutamylphos	hypothetical prote
AC1579	JC2410	T10742	H90094	B72314	139557	139559	GNNY1B	S34617	T16468	I47094	T27198	RDECER	D85513	F90662	F90497
~	C3	N	(7	0	C)	N	Н	ď	N	N	~	-1	N	N	7
188	303	390	446	471	485	486	2157	141	146	232	237	417	417	417	478
25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47	47	47	47	47	47	47	47
0	_	N	e	4	S	y 9	7	00	σ	0	41	c)	m	4	Ŋ

ALIGNMENTS

÷	RESULT 1 FO0337 PO19protein - infectious flacherie virus Cippecies: infectious flacherie virus A. Apprils Analysis of genetic information of an insect picorna-like virus, infectious flack flackers number: 214139; MUID:98166871; PMID:9505971 A. Actual virus infections A. Actual virus infectious flackers and the complex of
	C;Genetics: A;Gene: YPO3670 C;Superfamily: Escherichia coli hypothetical protein yhdP

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Gaps

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Risensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.I. Mol. Microbiol. 22, 175-191, 1996
Mol. Microbiol. 22, 175-191, 1996
Mylitle: Organizational characteristics and information content of an archaeal genome: 18, Reference number: S73076; WUID:97055432; PMID:8899719
A; Accession: S75372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9JRC7; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8540F
A;Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                                          A,Cross-references: UNIPROT:Q9ZW78; GB:AE002093; NID:g3763926; PIDN:AAC64306.1; GSPDB:GNC
C,Genetics:
A,Gene: At2g43170
A,Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccession: B81792
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable TonB-dependent receptor protein NMA2193 [imported] - Neisseria meningitidis (straces) - Neisseria meningitidis
C,Species: Neisseria meningitidis
C,Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P95944; EMBL:Y08257; NID:g1707772; PID:e283873; PID:g1707777 A;Experimental source: strain P2 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996 C;Genetics: A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein c04005 - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S75372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.5; DB 2; Length 137; Pred. No. 3; Mismatches 11; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: nucleic acid sequence not shown, translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                                          Length 504;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VIINELSOR-----DSCGPLKISLNNKILVYGN 30
                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                       Score 54; DB 2; Pred. No. 10; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.5; DE
Pred. No 17;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    266 QRTQSGPVTLQGNNNVM--GDMFSQATP 291
                                                                                                                                                                                                                                                                                                                                                      10 ORDSCGPLKISLNNKILVYGNLFSSFTF 37
                                                                                                                                                                                                                                          28.9%;
39.3%;
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Best Local Similarity 38.9%;
Matches 14; Conservative 4
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Best Local Similarity 40.0°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-137 <SEN>
                                                                         A; Residues: 1-504 <STO>
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                       A, Status: preliminary
A, Molecule type: DNA
A, Accession: H84862
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C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90518
R;Chambaud, I.; Hellig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90518
A;Accession: H90518
A;Accession: H90518
A;Molecule type: DNA
A;Residues: 1-1128
A;Molecule type: DNA
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Hypothetical protein At2g43170 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84862

R;In, X:; Raul, S: Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Alture 402, 761-768, 1999

A) Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Residues: 1.1128 «KUR»
A,Cross-references: UNIPROT:098024; GB:AL445566; PID:g14089629; PIDN:CAC13389.1; GSPDB:
A,Experimental source: strain UAB CTIP
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;
                                                                                                                                                              hypothetical protein ZK632.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: OcJan-1995 #sequence_revision O6-Jan-1995 #text_change O9-Jul-2004
C;Accession: S40938
R;Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1-619 <BER>
A,Residues: 1-619 <BER>
A,Cross-references: UNIPROT:P34652; EMBL:Z22181; NID:g297998; PID:g298004
C,Genetics: 117/3; 141/2; 256/3; 372/3; 428/1
C,Superfamily: calnexin
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                                                                                                                                                                                                                                                                                                                                  Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54.5; DE Pred. No. 21; 4; Mismatches
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                             ELSQRDSCGPLKISLNNKILVYGNLF 32
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1 Similarity 47.1%;
16; Conservative 4
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                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Lister of A, Reference number: $40933 A, A, Accession: $4093 A, Status: preliminary A, Molecule type: DNA
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nes 10; Conserv
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Best Local Similarity
Matches 16; Conserv
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C,Genetics:
A,Gene: MYPU 2160
A,Genetic code: SGC3
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Gaps

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Gaps

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Dipothetical protein SSO1294 [imported] - Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C; Accession: BSO284 R.S. Spo284 R.S. Supply, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Yong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. A.Pender to Genbank, April 2001 A.Pescription: Sulfolobus solfataricus complete genome.
                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-670 < DOU3
C;Genetics:
A;Gene: orf670
A;Map position: 1
A;Gene: nucleomorph
C;Keywords: nucleomorph
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-247 <KUR>
A,Cross-references: UNIPROT: Q97YM8; GB: AE006641; NID: gl3814496; PIDN: AAK41532.1; GSPDB: GP
C,Genetics:
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: T51044
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A;Molecule type: DNA
A;Residues: 1-461 <SCH>
A;Cross-references: UNIPROT:Q9P3J7; EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.140
A;Experimental source: BAC clone B15120; strain OR74A
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   A,Title: The highly reduced genome of an enslaved algal nucleus.
A,Reference number: A99082; MUID:11323671; PMID:11323671
A,Accession: G90091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 2; Length 247;
Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 INELSQRDSCGPL----KISLNNKILVYG----NLFSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 2
Pred. No. 20;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.5;
Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      28.3%;
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Best Local Similarity 35.77
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.6
Matches 15, Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SSO1294
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                                                                                RESULT 8
D81215
TonB-dependent receptor, probable NMB0293 [imported] - Neisseria meningitidis (strain MC c)species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81215
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Verstetence number: A81000; MUID:2017555; PMID:10710307
A;Reference number: A81000; MUID:2017555; PMID:10710307
A;Residues: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9JRC5; GB:AE002386; GB:AE002098; NID:g7225512; PIDN:AAF4074
C;Genetics:
A;Gene: NMB0293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein spr1195 [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae S;Streptococcus D; M; M; Arnold, J; Blaszczak, L; Burgett, S; DeHoff, B.S.; E R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J; Blaszczak, L.; Burgett, S;; DeHoff, B.S.; E R; N; B. Sun, P.M.; Winkler, M.E.
J; Bacteriol. 183, 5709-5717, 2001
A;Reference number: Aprong-Bellido, M; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Reterence number: B98021
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <KUR>
A;Cross-references: UNIPROT:Q8DPP1; GB:AE007317; PIDN:AAK99998.1; PID:g15458828; GSPDB:CC;Genetics:
C;Genetics:
A;Gene: spr1195
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(990091
hypothetical protein orf670 [imported] - Guillardia theta nucleomorph
c;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-011-2004
C;Accession: G90091
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53.5; DB 2; Length 7
Pred. No. 17;
4; Mismatches 15; Indels
AKVVEDKENPDRVG---IHLNNTSNVTGNLFFRYTP 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 AKVVEDKENPDRVG---IHLNNTSNVTGNLFFRYTP 622
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Best Local Similarity 38.9%;
Matches 14; Conservative
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A)Status: preliminary
A)Actocus bnA
A)Actocus bnA
A)Actocus bnA
A)Actocus bnA
A)Actocus bnA
A)Cross-references: UNIPROT:Q99TU2; GB:BA000018; PID:g13701350; PIDN:BAB42644.1; GSPDB:GR
C)Genetics:
A)Gene: pbp3
                                                                                                                                                                                                                26.7%; Score 50; DB 2; Length 691; ilarity 34.6%; Pred. No. 55; Conservative 7; Mismatches 10; Indels
A; Reference number: A89758; MUID: 21311952; PMID: 11418146
                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 10, 2004, 13:40:46 Job time : 9.24352 secs
                                                                                                                                                                                                                                                                                                                                      1 MAVIINELSQRDSCGPLKISLNNKIL 26
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Best Local Similarity
Matches 9; Conserv
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Development 125, 3343-3352, 1998
A;Title: A novel Dictyostellum cell surface protein important for both cell adhesion and A;Reference number: Z18798; MUID:98359946; PMID:9693138
A;Accession: T17456
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1402 <GIN>
A;Cross-references: UNIPROT:096668; EMBL:AF102575; NID:g4063398; PID:g4063399; PIDN:AAC9
A;Experimental source: strain Ax2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - phage SPP1

(5)Species: phage SPP1

(5)Species: phage SPP1

(5)Accession: T42238

R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.

Gene 204, 201-212, 1997

A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil

A;Reference number: 222137; MUID:98094274; PMID:9434185
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                                                                                                                                                                                                cell surface protein DTPA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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       Gaps
       3;
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A;Residues: 1-599 <ALO>
A;Cross-references: UNIPROT:048488; EMBL:X97918; PIDN:CAA66535.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 599;
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       Indels
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       11;
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Pred. No. 47;
5; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Wolecule type: DNA_____
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                                                                                           151 NRIGNREMYMNCAPVTIAANNKRDVAGAAFST 182
                                                 6 NELSQRD---SCGPLKISLNNKILVYGNLFSS 34
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illarity 33.3%;
Conservative 5
       Conservative
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Best Local Similarity
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Best Local Similarity
Matches 13; Conserv
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         12;
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         Matches
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Q6m621 corynebacte
Caf19856 corynebac
Q4zh9 ashbya goss
Q7zz9 xenopus lae
Q9dhr3 yaba-like d
Q867b0 can1s famil
Q86594 dictyostell
Q864ku8 brassica ol
Q84ku8 brassica ol
Q84ku8 brassica ol
Q84ky9 brassica ol
Q84ky9 brassica ca
 Q8ep29 oceanobacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=98166871; PubMed=9505971;
ISAWA H., Asano S., Sahara K., Ilzuka T., Bando H.;
"Analysis of genetic information of an insect picorna-like virus, infectious flacherie virus of silkworm: evidence for evolutionary relationships among insect, mammalian and plant picorna(-like)
                                                                                                                                                                                                                                                                                  DNA stage; Iflavirus.
                                                                                                                                                                                                                                                                                                                                                                                Arch. Virol. 143:127-143(1998).

R Arch. Virol. 143:127-143(1998).

EMBL; AB000906; BAA25371.1; -.

R GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003724; F:RNA binding; IEA.

GO; GO:0003724; F:RNA helicase activity; IEA.

GO; GO:0003903; F:RNA-lirected RNA polymerase activity; IEA.

GO; GO:0009079; F:RNA-lirected RNA polymerase activity; IEA.

R GO; GO:0019079; F:RNA-lirected RNA polymerase activity; IEA.

R InterPro; IPR000605; RNA-helicase.

R InterPro; IPR001095; RNA-pol_BS PS.

R InterPro; IPR001094; RNA-pol_PS'ir.

R InterPro; IPR001094; RNA-pol_PS'ir.

R FinerPro; IPR008975; Viral_cap_coat.

R Ffam; PF00809; RNA-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 59; DB 2; Length 3085; 34.1%; Pred. No. 80; ive 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 ISLNELTERYIVIANGVLTSGDTRGQVKFSLDLPAAIYGNLDSS 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3085 AA; 345800 MW; 23FC9600DBF71531 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                               Polyprotein.
Infectious flacherie virus.
Viruses; ssRNA positive-strand viruses, no
NCBI_TaxID=12742;
                                                                                                                                                            ALIGNMENTS
                  O6M621
CAF19856
Q74ZH9
AAS54713
Q7ZZZ9
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                                                                    Q9DHR3
Q867B0
Q867G4
Q9PYW1
Q84KU8
Q84KY9
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  000000000000000
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Best Local Similarity 34.1
Matches 15, Conservative
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                                                                                                                                                                                                              PRELIMINARY;
523
755
971
1321
1321
617
617
812
812
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8423
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Polyprotein.
SEQUENCE
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Arch. Virol
 Q9M877;
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Q9M877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             098qz4 mycoplasma
083v23 pseudomonas
082w78 arabidopsis
094a14 arabidopsis
09544 sulfolobus
095k2 neisseria m
07ax11 neisseria m
091px1 neisseria m
091rc5 neisseria m
091rc7 neisseria m
091rc7 neisseria m
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P34652 caenorhabdi
Q6cdd3 yarrowia li
Q84kv6 brassica ol
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9m877 arabidopsis
Q86k14 dictyosteli
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Q8zaw2 yersinia pe
Aas64021 yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6cps0 kluyveromyc
Q9pyz6 xestia c-ni
Q8dpf1 streptococc
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guillardia
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sulfolobus
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                                                                    November 10, 2004, 12:27:34 ; Search time 45.1796 Seconds (without alignments) 471.205 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                          Description
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Q98rt4
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Q97ym8
Q7tsf9
                                                                                                                               MAVIINELSQRDSCGPLKISLNNKILVYGNLFSSFTP 37
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 residues
                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                         070710
09M877
086K14
08B1P4
08ZAW2
AAS64021
POLG HRV16
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OSDPF1
OR42 MOUSE
O9P930
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Maximum Match 1008
Listing first 45 summaries
                                                  protein search, using sw model
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0980Z4
0934Z3
094A14
094A14
090PK2
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090PK3
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090PK3
090PK3
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Q97YM8
Q7TSF9
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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187
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Match
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Perfect score:
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Maximum DB
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SEQUENCE FROM N.A.
STRAIN-KIMS, / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.W., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.W., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.W., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=91001 / Biovar Mediaevalis; Song Y., Tong Z., Wang J., Zhou Song Y., Tong Z., Wang L., Han Y., Zhang J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.;
                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.5%; Score 57; DB 2; Length 1063; Best Local Similarity 50.0%; Pred. No. 50; Matches 13; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1063 AA; 116550 MW; B05D377F05653039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRZAWZ; Q74PMZ;
01-MAR-2002 (TTEMBLrel. 20, Created)
01-MAR-2002 (TTEMBLrel. 20, Last sequence update)
01-0CT-2004 (TTEMBLrel. 28, Last annotation update)
Putative exported protein.
OrderedLocusNames=YP3876, YPO3670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1307 AA
                                                                                                                                                                                                                                                                                                                                                                           "Genôme sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
BMEL; AE013619; AAM83789:1; -.
Hypothetical protein:
SEQUENCE 1063 AA; 116550 MW; B05D377F05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ELSQRDSCGPLKISLNNKILVYGNLF 32
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STRAIN=CO-92 / Biovar Orientalis;
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                                                                                                             Yersinia pestis.
                                                                                                                                                                    NCBI_TaxID=632;
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Q8ZAW2
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                                                                                                                                            LIN X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
A Din X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
A Ronning C.M., Koo, H., Pujii C.Y., Utterback T.R., Barnstead M.B.,
Bowman C.L., White O., Nierman W.C., Traser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, ACO2184015 APR32472.1;
InterPro; IPR002885; PPR.
R InterPro; IPR002885; PPR.
R InterPro; IPR00215; Prot_inh_serpin.
R Pfam; PF03140; DUF247, 1.
R Pfam; PF03140; DUF247, 1.
R TIGRPAMS; TIGR00756; PPR; 7.
R TIGRPAMS; TIGR00756; PPR; 7.
R SEQUENCE 1077 AA; 121922 MW; 4A8FIFE09A8DC7AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids,
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-010-2003 (TrEMBLrel. 24, Created)
01-010N-2003 (TrEMBLrel. 24, Last sequence update)
01-01NR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Gpl38.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumgart C.;
Submitted (MAR-2003) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AC116984; AAO51312.1; -.
SEQUENCE 660 AA; 73846 MW; 3E8341398E7A6CB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Best Local Similarity
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Local S....
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Q86K14

RESULT 3
1086K14
1006K14
1001-906K
DT 01-91-01-01
DE 01-01-01
DE 0

Matches

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Gaps

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Zhou D.,

1307 AA; 144414 MW; F2C5A282B066CE54 CRC64;

PRT; 1063 AA

PRELIMINARY;

Q8D1P4 Q8D1P4;

RESULT 4 Q8D1P4

Matches

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Structure 1:51-68(1993).
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ProDom;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2004 (Rel. 45, Last amnotation update)
01-OCT-2004 (Rel. 45, Last amnotation update)
Genome polyprotein [Contains: Caat protein VP4 (PlA); Coat protein VP2 (PlB); Coat protein VP2 (PlB); Coat protein PP2, Core protein PP3, Gore protein PP3, Gore protein PP3, Gore protein PP3, Genome-linked protein VPG (PBB); Picornain 3C (EC 3.4.22.28) (Protease 3C) (PP3); RNA-directed RNA polymerase (EC 2.7.7.48) (PB3)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
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MEDLINE=95250310; PubMed=7732663;
Lee W.M., Wang W., Rueckert R.R.;
"Complete sequence of the RNA genome of human rhinovirus 16, a
clinically useful common cold virus belonging to the ICAM-1 receptor
                                                                    Gaps
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MEDLINE=94348864; PubMed=7915182;
Oliveira M.A., Zhao R., Lee W.M., Kremer M.J., Minor I.,
Rueckert R.R., Diana G.D., Pevear D.C., Dutko F.J., McKinlay M.A.,
Rossmann M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
NCBI_TaxID=632;
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STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou Han Y., Pang X., Zhai J., Chen F., Oun H., Wang J., Li S., Guo Z. Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.,
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      DB 2; Length 1307;
62;
                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017142; AAS64021.1; -.
SEQUENCE 1307 AA; 144414 MW; F2C5A282B066CE54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                      24-WAR-2004 (TrEMBLrel. 27, Created)
24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 PRT; 1307 AA
                                                           3; Mismatches
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         Score 57;
Pred. No. 6
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         30.5%;
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Virus Genes 9:177-181(1995).
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   Query Match
Best Local Similarity 50.0'
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia pestis.
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POLG HRV16
ID POLG HRV16
AC Q82122;
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AAS64021;
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RD SEQUENCE FROM N.A.

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RC STRAIN=Bristol N2;

RX MEDIJURS-94150718; bubMed=7906398;

RA Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,

RA Gratton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Pulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Fulton L., Jones M., Kershaw J., Kirsten J., Laisster N.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,

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RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Volandam M.,

RA Sins M., Smaldon N., Smith A., Sonnhamer E., Staden R.,

RA Sins M., Smaldon N., Smith A., Meinstock L., Wilkinson-Sproat J.,

RA Wohldman P.,

RA Wohl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                Score 56.5; DB 1; Length 2153;
Pred. No. 1.3e+02;
8; Mismatches 6; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 NELSQRD--SCGPLKI----SLNNKIL---VYGNLFSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
CCalnexin homolog precursor.
ORFNames=ZK632.6,
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                   30.2%;
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Best Local Similarity 41.0°
Matches 16; Conservative
   CAEEL
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    RNA-directed RNA polymerase.
N-myristoyl glycine (by host).
Protease (Potential).
Protease (Potential).
KD -> NH (in Ref. 1).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDIJEB-222866392; PubMed=12399400;
SALD.INB-222866392; PubMed=12399400;
SALD.INB-222866392; PubMed=12399400;
Ockendon D.J., Satta Y.;
"Coevolution of the S.locus genes SRK, SLG and SP11/SCR in Brassica clerace and B. rapa ";
Genetics 162:931-940(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 29.1%; Score 54.5; DB 2; Length 438; Local Similarity 40.6%; Pred. No. 45; les 13; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                    Length 1914;
                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                   NON TER 1 1 1 SEQÜENCE 1914 AA; 220365 MW; 1DE84B605332F9ED CRC64;
                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49636 MW; 93452E2A7BE2008E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                             .Match
Local Similarity 46.9%; Pred. No. 1.8e+02;
iss 15; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAVIINELSORDSCGPLKISLNNKILVYGNLF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LSIYINTLSSRES---LKISSNRTLVSPGSIF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                    5 INELSORDSCGPLKISLNNKIL--VYGNLFSS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1128 AA.
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InterPro; IPR003609; Pan app.
IPRMT; SM00168; B lectin; 1.
PRMAT; SM00108; B lectin; 1.
PROSITE; PS50927; BUIL LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
S-locus receptor kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea (Cauliflower)
                                                                                                                                            Genoscope;
Submitted (JUL-2004) to the
EMBL; CR382129; CAG81624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                        Nature 430:35-44 (2004)
"Genome evolution in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA;
                                                                                    SEQUENCE FROM N.A. STRAIN=CLIB99;
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Q98QZ4;
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Q98QZ4
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Boinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 619 Calnexin homolog. .) (Potential). 203 203 N-linked (GIGNAc. .) (Potential). 571 N-linked (GIGNAc. .) (Potential). 619 AA; 69207 MW, 08903CE519A75E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to tr|Q9UVK9 Yarrowia lipolytica Fkslp (Fragment).
ORFNames=YALIOCO1411g;
Varrowia lipolytica (Candida lipolytica).
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; P34652; -.

R Interpro; PR001580; Calret/calnex.

R Interpro; IPR001580; Calret/calnex.

R Interpro; IPR001583; Calret calnex.

R Interpro; IPR001898; Conhalike lec_gl.

R PRINTS; PR00656; Calreticulin; 1.

R PROSTE; PS00805; Calreticulin; 2.

R PROSTE; PS00805; Calreticulin; Repeat; 1.

W Hypothetical protein; Lectin; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 55; DB 1; Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
reticulum (By similarity). SIMILARITY: Belongs to the calreticulin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
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                                                                                                                                                                                                                                                                                              EMBL, 222181; CAA80183.1; -. PIR; 540938; 540938. HSSP; P18418; 1K9C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 43.5
ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouchier C., Caudron B.,
Wincker P., Souciet J.L.;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicacees, Arabidopsis.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Cheuk R., Chan H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hauan V.W.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Subunsley S.D., Jin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Romning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Koesema 2., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
Banh J., Boweer L., Carrinci P., Dale J.M., Goldsmith A.D.

Hayashizaki Y., Ishida J., Jang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick P.

Tang C.C., Torliumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theelogis A., Ecker J.R.,

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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      Indels
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Trown C.D., Kaul S.)
Submitted (FES-2002)
EMBL, AC004450, AAC64306.1)
FIR, H84862, H84862.
HYDOCHETICAL Protein Protein
SEQUENCE 504 AA; 52252 MW; 8B6E7FD3D6F100FB CRC64;
                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein At2943170.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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      Mismatches
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6; Mismatches
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1 Similarity 39.3%; Pred. No. 4
11; Conservative 6; Mismatci
                                                                                                      124 GALKVRFSNSVLKYGNOFMS 143
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                                                                 15 GPLKISLNNKILVYGNLFSS
   10; Conservative
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Best Local Similarity
Matches 11; Conserv
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01-DEC-2001
01-DEC-2001
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      Matches
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Q94A14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wypulist, MYPU-2160; -. Gold-400, Fiphospholipase C activity; IEA. Gold-4004432; Fiphospholinositide phospholipase C activity; IEA. Gold-60000422; Pihtoseplular signaling cascade; IEA. Gold-60006629; Pilipid metabolism; IEA. InterPro: IPRO01326; Lipoprotein.17.
InterPro: IPRO01326; Lipoprotein.17.
Pfam; PF04200; Lipoprotein.17; 4.
PROSITE: PSSO008; PIPLC Y EDMAIN; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 1128 AA; 127054 MW; 56D54050D0742EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                       Mycoplasma pulmonis.
Bacteria<u>i Firmi</u>cutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                         MEDLINE=21267165; PubMed=11353084; Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Gal Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C. Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 412;
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EMBL; AB088043; BAC65314.1, -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005741; C:mitcchondrial outer membrane; IEA.
GO; GO:0005818; F:porin activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005318; OprD.
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein MYPU_2160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 54.5; DB
; Pred. No. 1.2e+
4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma pulmonis.",
Nucleic Acids Res. 29:2145-2153(2001).
EMBL, AL445563; CAC13389.1; -.
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                                                                                                                             OrderedLocusNames=MYPU_2160;
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Pseudomonas fluorescens.
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SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                                                   NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                  STRAIN=UAB CTIP;
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Query Match

Matches

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Q83V23; Q83V23

RESULT 12
1083V23
AC 083V2
AC 083V2
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STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726;

A Mayez M.J. Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Mayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A De Moors A., Erauso G., Fletcher C.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Raddar P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",

RTHE COMPLE SGI. U.S.A. 98:7835-7840(2001).

SR EMBL, AR06551; AAK40472.1; -.

DR PIR, S75372.

SR EMBL, AR06551; AAK40472.1; -.

SR EMBL, AR06551; AAK40472.1; -.

SR Complete protecome, Hypothetical protein.

SR SEQUENCE I37 AA, 15479 WW; BBB29552844F6110 CRC64;
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Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
LSubmitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
REMBL; AY050457; AAK91471.1; -.
REMBL; BT002247; AAK91471.1; -.
REMBL; BT002247; AAK91471.1; -.
REMBL; PR00339; IEDU.
RICEPPO; IPR001026; Epsin N.
RICEPPO; IPR001026; Epsin N.
RICEPPO; IPR008943; PL bind N.
REMBL; SM0273; BNTH; 1.
REMBL; PS50942; ENTH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
0rf c04005 protein (Hypothetical protein SSO0117).
0rf c04005, OrderedLocusNames=SSO0117;
Sulfolobus solfatarious, Thermoprotei; Sulfolobales; Sulfolobaceae;
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(7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.9%; Score 54; DB 2; Length 895; 39.3%; Pred. No. 1.1e+02; ive 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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40.0%; Pred. No. 18;
ive 3; Mismatches
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STRAIN=P2;
MEDLINE=97055432; PubMed=8899719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 39.3,
Best Local 11, Conservative
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Matches 14; Conservative
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NCBI_TaxID=2287;
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P95944;
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P95544
AC P9594,
AC P9594,
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Search completed: November 10, 2004, 13:38:41 Job time : 47.1796 secs This Page Stank Misoto,

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Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

November 10, 2004, 12:32:37; Search time 5.52677 Seconds (without alignments) 191.991 Million cell updates/sec Run on:

US-10-092-750-39 84 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GLAKKSKRNPANLTPP 16 Scoring table:

478139 segs, 66318000 residues Searched:

478139 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	47 Sequence 197	e 14	equence 14	equence 14	11 S	6 Sequence 45	4 Seguence 45'	81 Sequence 249	equence 8,	equence 22	28 Sequence 26	7	equence 1, Ap	24 Seguence 30524	equence 2, Ap	9 Sequence 43029	39, A	0 Sequence 38270	7 Seguence 53487	Sequence 4296,	99 Sequence 20599	28 Sequence 32728	. 5352	8 Seguence 42648	968	29 Seguence 24429	Seguence 27
SUMMARIES	ŒΙ	-09-2	-04	77-1	US-10-222-578-14	-991A-	-270-767-454	-09-270-7	2-991A-24	-269-731	-896-7	-248-796A-26	٩		09-252-991A	-09-896-72	-09-270-767-	9-724-864-	-09-270-767-382	-09-270-767-5	-09-328-352-429	9-248-796A-20	52-991A-32	~	-09-270-767	-09-732-210-96	-248-79	-199-637A-27
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Sequence 21632, A	Sequence 16827, A	Sequence 43724, A	Sequence 2, Appli		Sequence 6776, Ap	Seguence 7430, Ap	Sequence 2, Appli	Seguence 41531, A	Sequence 2, Appli	Seguence 1821, Ap	Seguence 1821, Ap	Seguence 1821, Ap	Seguence 172, App	Seguence 172, App	Seguence 783, App		Sequence 172, App	
US-09-248-796A-21632	US-09-252-991A-16827	US-09-270-767-43724	US-09-492-308A-2	US-09-328-352-4778	US-09-107-532A-6776	US-09-543-681A-7430	US-09-492-985-2	US-09-270-767-41531	US-08-532-896-2	US-09-702-705-1821	US-09-736-457-1821	US-09-671-325-1821	US-09-643-597-172	US-09-480-884A-172	US-09-702-705-783	US-09-736-457-783	US-09-542-615A-172	
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157	170	178	181	196	233	276	288	294	323	323	323	323	364	364	364	364	364	١.
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28	53	30	31	32	33	34	35	36	37	38	ტ ტ	40	41	42	43	44	45	

ALIGNMENTS

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Sequence 19247, Application US/09248796A
| Sequence 19247, Application US/09248796A
| Sequence 19247, Application US/09248796A
| Patent No. 6747137
| GENERAL INFORMATION:
| APPLICANT: Keith Neinstock et al
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
| TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 107196.132
| CURRENT APPLICATION NUMBER: US 60/074,725
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-08-13
| NUMBER OF SEQ ID NOS: 28208
| SEQ ID NOS: 28208
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Pred. No. 38;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 46.2
Matches 6; Conservative
RESULT 1
US-09-248-796A-19247
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VS-09-045-14

VS-09-045-14

VS-09-045-14

Sequence 14, Application US/09790045

PEtent No. 6495210

GENERAL INFORMATION:

APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Horita, Mitsuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum

PETER REFERENCE: NAN-106US

CURRENT APPLICATION NUMBER: US/09/790,045

CURRENT FILING DATE: 201-02-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0

LENGTH: 274

LENGTH: 274

CURRENT: 274

CORGANISM: Ralstonia solanacearum |: ::||: ||| 12 KRKRKNPSTTTPP 24 d

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RESULT 6
8-09-270-767-45426
; Sequence 45426, Application US/09270767
; Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20111
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13 LARKTKRYPSDLT 25
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Best Local Similarity 58.3
Matches 7; Conservative
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Matches 7; Conservative
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                                                                           RESULT 5
US-09-252-991A-20111
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Sequence 14, Application US/10222577

Sequence 14, Application US/10222577

SERENAL INCRMATION

APPLICANT: Hassbe, Akira

APPLICANT: Horita, Mitsuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia

FILLE REPRENCE: NAND108015

TITLE OP INVENTION: Solanacearum

FILLE REPRENCE: NAND108015

CURRENT APPLICATION NUMBER: US/10/222,577

CURRENT FILING DATE: 2002-08-16

FRICR APPLICATION NUMBER: US/09/790,045

FRICR FILING DATE: 201-02-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0
                                                                               Gaps
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APPLICANT: Hasebe, Akira
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
Patent No. 657007
TITLE OF INVENTION: Solanacearum
FILE REFERENCE: NANPLOBUS
CURRENT APPLICATION NUMBER: US/10/222,578
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/790,045
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
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                                     Score 42; DB 4; Length 274; Pred. No. 32; 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-222-578-14
; Sequence 14, Application US/10222578
; Patent No. 6570007
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Ralstonia solanacearum
US-10-222-577-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Ralstonia solanacearum
US-10-222-578-14
                                       50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LAKKSKRNPANLT 14
                  Query Match
Best Local Similarity 61...
Best Local 81, Conservative
                                                                                                                                            ||:|:|| |::||
13 LARKTKRYPSDLT 25
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                                                                                                                       2 LAKKSKRNPANLT 14
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Matches 8; Conservative
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SEQ ID NO 14
LENGTH: 274
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US-10-222-577-14
    US-09-790-045-14
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LENGTH: 274
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DP
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Sequence 2011. Application US/09252991A

Sequence 2011. Application US/09252991A

Sequence 2011. Application US/09252991A

Sequence 2011. Application GEST/95

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION WINDER:
US/09/252,991A

CURRENT APPLICATION WINDER:
US/09/252,991A

CURRENT FILING DATE:
1999-02-18

PRIOR APPLICATION WINDER:
US/00/74,788

PRIOR APPLICATION WINDER:
US/00/74,788
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44426
LENGTH: 427
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Sequence 45764, Application US/09270767

Sequence 45764, Application US/09270767

GENERAL INFORMATION:

APPLICANT: HOMBURISER et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
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Pred. No. 46;
4; Mismatches 1; Indels
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us-10-092-750-39.raı
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RESULT 11
10.09-248-26528
1 Sequence 26528, Application US/09248796A
2 Sequence 26528, Application US/09248796A
3 Patent No. 6747137
1 GENERAL INFORMATION:
3 TELLOWER SECTION OF THE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
3 TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION NUMBER: US/09/269,731
FILING DATE: WO FR97/01768
FILING DATE: WO FR97/01768
FILING DATE: OCCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 96 12204
FILING DATE: OCCT-1996
ATTORNEY/AGBNT IPPORMATION:
FILING DATE: OCCT-1996
ATTORNEY/AGBNT IPPORMATION:
REGISTRATION NUMBER:
FILING DATE: OT 01-155
TELEPRAX: (703) 412-1161
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid

CS-09-731-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.8%; Score 41; DB 3; Length 545; S0.0%; Pred. No. 95; tive 4; Mismatches 4; Indels
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US-09-896-720-22

i Sequence 22, Application US/09896720
; Patent No. 6780657
; GENERAL INFORMATION:
    APPLICANT: SONG, WEN-YUAN
; APPLICANT: PI, LI-YA
TITLE OF INVENTION: UBIQUITIN LIGASE
; FILE REFERENCE: 583-173
CURRENT APPLICATION NUMBER: US/09/896,720
CURRENT FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2000-06-29
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PATENT ON UNCT: 2.1
; SEQ ID NO 22
LENGTH: 50
; TYPE: PRT

TYPE: PRT

TYPE: PRT
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Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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Sequence 24981, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINGAR FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-28
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24981

LENGTH: 400
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Pred. No. 1.3e+02;
1; Mismatches 2; Indels
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48.8%; Score 41; DB 4; Length 400;
Best Local Similarity 46.7%; Pred. No. 69;
Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                   , TYPE: PRT
, ORGANISM: Drosophila melanogaster
US-09-270-767-45764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORGANISM: Pseudomonas aeruginosa US-09-252-991A-24981
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:: :|:||
127 LARRRQRDPAGAQPP 141
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45764
LENGTH: 1059
                                                                                                                                                                                                                                                                                                                                                                                                                       :| | |||||
456 RRKPQNLTPP 465
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ORGANISM:
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Parent No. 6551795

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT: MACO J. RUBENCE ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PLILING DATE: 1988-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30524

LENGTH: 171

SEQ ID NO 30524
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MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastGEG for Windows Version 2.0
SOFTWARE: FastGEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewith
FLING DATE: Filed Herewith
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY-AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELEPHONE: 416-855.0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.6%; Score 40; DB 4; Best Local Similarity 50.0%; Pred. No. 42; Matches 7; Conservative 4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2;
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09896720 ; Patent No. 6750057
                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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81 ACRSRRNPGSPSPP 94
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US-09-252-991A-30524
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; ORGANISM: Pseudor
US-09-252-991A-30524
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US-09-896-720-2
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TITLE OF INVENTION: DEPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 5657
LENGTH: 112
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Sequence 1, Application US/08829110

Patent No. 5882890

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

APPLICANT: Goll, Surya K.

TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN

TITLE OF INVENTION: SIGNALING

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
CURRENT PALLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PLICATION NUMBER: US 60/096,409
PRIOR PLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 26528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive CITY: Palo Alto
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                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Candida albicans
US-09-248-796A-26528
                                                                                                                                                                                                                                                                                                                                                                                                                 3 AKKSKRNPANLTP 15
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ZIP: 94304
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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GENERAL INFORMATION:
APPLICANT: SONG, WEN-YUAN
FAPLICANT: SPT, LI-Y
TITLE OF INVENTION: UBIOUTIN LIGASE
FILE REFERENCE: 5853-173
CURRENT APPLICATION WUMBER: US/09/896,720
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/215,049
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
SOFTWARE: Patentin Ver. 2.1
SOOTWARE: Patentin Ver. 2.1
SEQ ID NO 2
SEQ ID NO 2
SOTWARE: Patentin Ver. 2.1
SEQ ID NO 2
SOTWARE: Patentin Ver. 2.1
SEQ ID NO 2
SOTWARE: PATENTIN (258)
LUCCATION: (258)
COCATHER INFORMATION: Any amino acid
US-09-896-720-2
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Search completed: November 10, 2004, 13:44:10 Job time: 6.52677 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:	November 10, 2004, 16:36:12; Search time 17.1883 Seconds (without alignments) 328.807 Million cell updates/sec
Title: Derfact score:	US-10-092-750-39 84
Sequence:	1 GLAKKSKRNPANLTPP 16
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	1566620 segs, 353225886 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/Der NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Sequence 39, Appl	Sequence 3417, Ap	Sequence 211273,	Seguence 228508,	Sequence 64638, A	Sequence 250313,	Sequence 211116,	Sequence 191510,	Sequence 168814,	Sequence 253454,	Sequence 335386,	Seguence 306150,	Sequence 353683,
	Ω		US-10-092-750-39	US-10-264-049-3417	US-10-425-115-211273	US-10-425-115-228508	US-10-425-114-64638	US-10-425-115-250313	US-10-424-599-211116	US-10-425-115-191510	US-10-424-599-168814	US-10-425-115-253454	US-10-425-115-335386	US-10-425-115-306150	US-10-425-115-353683
	DB		14	15	17	17	15	17	15	17	15	17	17	17	17
	Query Match Length DB	1	16	23	94	143	324	446	184	538	170	109	160	247	81
ф	Query	1	100.0	73.8	57.1	56.0	56.0	56.0	54.8	54.8	53.0	52.4	52.4	52.4	51.8
	Score		84	62	48	47	47	47	46	46	44.5	44	44	44	43.5
	Result No.	1 1 1 1	П	01	m	4	Ŋ	9	7	80	6	10	11	17	13

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7 US-10-437-963-16975 7 US-10-425-115-27985 7 US-10-425-115-27700 8 US-10-425-115-27700 10S-10-425-115-27700 10S-10-425-115-27895 10S-10-425-115-27895 10S-10-425-115-27895 10S-10-425-115-27895 10S-10-425-115-27895 10S-10-427-1284-6595 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-2875 10S-10-425-115-287310 10S-10-425-115-287310 10S-10-425-115-288-203-88	7 US-10-425-115-1903 6 US-10-437-963-1952
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100.0%; Score 84; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
US-10-092-750-39

US-10-092-750-39

Sequence 39, Application US/10092750

Publication No. US20030032157A1

GENERAL HORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Hammond, Philip W.
TILE REFERENCE: 50036/050002

TILLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT APPLICATION NUMBER: US 60/274,526

PRIOR PILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PastSEQ for Windows Version 4.0

LEAST APPLICATION NUMBER: US/10/10-08

SEQ ID NO 39

LEAST APPLICATION NUMBER: US/10/10-08

MUMBER OF SEQ ID NOS: 253

SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-39
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1 GLAKKSKRNPANLTPP 16 1 GLAKKSKRNPANLTPP 16 à

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; Sequence 3417, Application US/10264049; Publication No. US20040005579A1; GENERAL INFORMATION: RESULT 2 US-10-264-049-3417

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Squence 64638 Application US/10425114

(Squence 64639, Application US/10425114

(Squence 64639, Application US/10425114

(Squence 64638, Application US/20040034888A1

(Squence 64638, Application No. US2004003488BA1

(Squence 1, Juny Applicant: Liu, Jingdong

(APPLICANT: Expense)

(APPLICANT: Screen, Steven E

(APPLICANT: Tabaska, Jack E

(APPLICANT: Cao, Yongwei

(TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

(TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

(CURRENT APPLICANTION NUMBER: US/10/425,114

(CURRENT APPLICANTION NUMBER: US/10/425,114
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Publication No. US20040214272A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Avoid K.
APPLICANT: Avoid K.
APPLICANT: Avoid K.
APPLICANT: Avoid K.
APPLICANT: Prongred
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 256313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: UC-ZMFLB73159D10_FLI.pep
US-10:425-114-64638
                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_139992C.1.pep
US-10-425-115-228508
                                                                                                                                                                                                                                                                                                                                                          Score 47; DB pred, No. 20; Mismatches
   FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 228508
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                             56.0%;
81.8%;
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Best Local Similarity 81.8.
Local Similarity 91.8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 SKPNPATLTPP 107
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                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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; Sequence 211273, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 211273
; LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-3417
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Availc, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nooleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nooleic
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HAPPLICANT: Birse et al.

ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAl33P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.8%; Score 62; DB 15; Length 23; Best Local Similarity 75.0%; Pred. No. 0.015; Matches 12; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_124277C.1.pep
US-10-425-115-211273
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Zea mays
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US-10-425-115-228508
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Usello-253454

Sequence 253464, Application US/10425115
Sequence 253464, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expurity David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE REPERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 253454
                                                                         Gaps
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   Length 538;
                                                                         4; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_123454C.1.pep
US-10-424-599-168814
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US-10-425-115-253454
Query Match
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 4
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                                                                                                                                              2 LAKKSKRNPANLTPP 16
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ORGANISM: Zea mays
FEATURE:
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US-10-424-599-211116
US-10-424-599-211116
Sequence 211116, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rowalt David K
APPLICANT: Cav Yihua
APPLICANT: Cav Yorogwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
EENGTH: 184
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| Sequence 101510, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INPORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: La Rovalic, David K.
| APPLICANT: Zhou, Yihna
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: David K.
| TITLE OF INVENTION: ADALICATION NUMBER: US/10/425,115
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 191510
| LENGTH: 538
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US-10-424-599-211116
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106236C.1.pep
US-10-425-115-191510
                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_159873C.1.pep
US-10-425-115-250313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 15;
Pred. No. 37;
3; Mismatches 3.
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LOCATION: (1)..(184)
PERTION: unsure at all Xaa locations
FEATURE:
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Best Local Similarity 53.8%;
Matches 7; Conservative
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24 KKKKKNPKKISPP 36
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          ORGANISM: Zea mays
                                           FEATURE:
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Sequence 353683, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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7 GIPRKSQR-PLSLTPP 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 353683
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                                                                                                                                                                                                       Sequence 335386, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Soc., Thomas J.
APPLICANT: Enou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Soc., Younger
APPLICANT: Chou, Yihua
APPLICANT: Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

APPLICANT: Broad, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

PILE REPERBECE: 38-21 (5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

WUMBER OF SEQ ID NOS: 369326

SEQ ID NO 36150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.4%; Score 44; DB 17; Length 247; 50.0%; Pred. No. 1e+02; Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_68982C.1.pep
US-10-425-115-335386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION; Clone ID: MRT4577_42272C.1.pep
US-10-425-115-306150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(160)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
1 GLAKKSKRNPANLTPP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GFLLRSHRNPSKLLPP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 KKKKKNPPNPFPP 28
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Best Local Similarity 50.0°
....hes 8; Conservative
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FEATURE:
                                                                                                                                                                                               US-10-425-115-335386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
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US-10-425-115-306150
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RESULT 13

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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei, Wei
APPLICANT: Wu, Wei, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169759
LENGTH: 66
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Y. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBURS: 38-21(5322)B
FURE REPERBURS: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Pred. No. 38;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: PAT_MRT4530_68148C.1.pep
US-10-437-963-169759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Clone ID: MRT4577_85733C.1.pep US-10-425-115-353683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 43.5; D
56.2%; Pred. No. 39;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 169759, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS-10-425-115-279854

Sequence 279854, Application US/10425115

PUBLICATION No. US20040214272A1

SENEMAL INFORMATION:
RAPPLICANT: La Rosa, Thomas J.
```

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## APPLICANT: Kovalic, David K.

### APPLICANT: Zhou, Yihua

### APPLICANT: Zhou, Yihua

### APPLICANT: Zhou, Yihua

### APPLICANT: Zhou, Yihua

### APPLICANT: Cao, Yongwei

### TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

### TITLE OF INVENTION: Plants

### TITLE OF INVENTION: Plants

### CURRENT APPLICATION NUMBER: US/10/425,115

### CURRENT APPLICATION NUMBER: US/10/425,115

### CURRENT PILING DATE: 2003-04-28

### CURRENT PILING DATE: 2003-04-28

### TYPE: PRT

### ORGANISM: Zea mays

### CURRENT PRATURE:

#### OTHER INFORMATION: Clone ID: MRT4577_186806C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLAKKSKRNPANLTPP 16
|:||| |:
|18 GVAKKKKKKKKKTPP 133
```

Search completed: November 11, 2004, 01:28:21 Job time: 18.2383 secs

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The Book of Mary Copy

us-10-092-750-39.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 10, 2004, 12:29:32 ; Search time 3.56477 Seconds (without alignments) 431.857 Million cell updates/sec

US-10-092-750-39 84 1 GLAKKSKRNPANLTPP 16 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ok				
Result No.	Score	Query	Length	DB	ID	Description
, ਜ ਜ :	44	i N	306	. 2	867131	hypothetical prote
7	43	51.2	1171	N	T31635	hypothetical prote
m	42	0	409	7	S70704	carbon catabolite
4	42	50.0	419	7	T10652	ical
Ŋ	42	0	57	N	F81866	ĸ.
v	42	50.0	57	N	F81075	RNA
7	42	0	103	N	T14124	
80	41.5	g	72	~	S67044	NFI1 protein - yea
σ	41		268	N	G02133	-amo
10	41	48.8	269	~	T26823	hypothetical prote
11	41		280	N	D86193	Н
13	41		281	~	T45926	Н
13	41		565	N	H69363	~
14	4.1		629	N	B82545	u
15	41		777	~	830271	_
16	41		843	N	833442	1
17	41	48.8	1822	0	S33441	EF protein - Strep
18	40		116	N	E72622	Н
19	40		164	~	A85063	hypothetical prote
20	40		212	N	A84971	_
21	40	•	346	N	AC3108	hypothetical prote
22	40		371	N	A98179	╁
23	40	47.6	374	Н	TXXXTX	beta-lytic metallo
24	40	•	567	N	AG2008	hypothetical prote
25	40	47.6	683	N	T34103	hypothetical prote
56	40	•	697	N	C75525	/bdopterin_o
27	40	47.6	720	N	~	ABC transporter-li
28	40		1122	N	5	exiT protein - Myc
59	40	47.6	2252	N	S06188	genome polyprotein

hypothetical prote	hypothetical prote	FMRFamide-like pep	lysozyme (EC 3.2.1	hypothetical prote	glycoprotein gp63	hypothetical prote	probable salt-indu	probable arginyl-t	transcription fact	transcription fact	glycyl-tRNA synthe	hypothetical prote	hypothetical prote	F13B4.4 protein -	hypothetical prote
T50315	E75077	T26262	AD3322	T47760	VGBE63	E71677	D84778	T36252	839356	S61977	AB1257	T27402	S57157	E86268	T52517
73	N	Ŋ	7	7	Н	N	N	~	~	7	7	7	7	7	73
780	118	184	277	298	350	415	497	586	644	979	688	969	707	786	929
47.0	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4	46.4
39.5	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
30	31	32	33	34	35	36	37	38	ტ ტ	40	41	42	43	44	45

ALIGNMENTS

C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004	
R; Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; D	Α., υ
A; Cross-references: UNIPROT: Q08634; EMBL: 275146; NID: 91420544; PID: 91420545; GSPD	GSPD
Thierry Thierry::914205	7, i

DB:GN0001

Dujon, B.

A; Map position: 15R

Gaps ; Query Match 52.4%; Score 44; DB 2; Length 306; Best Local Similarity 60.0%; Pred. No. 13; Matches 9; Conservative 0; Mismatches 6; Indels

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253 LTKKRSKNPFNRTAP 267 2 LAKKSKRNPANLTPP 16 g

hypothesical protein YS7A10A.m - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Space: 29-0cr-1999 #text_change 20-Jun-2000
C;Accession: T31635
R;Smye, R.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z21048
A;Recession: T31635
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Recence type: DNA
A;Residues: 1-1171 <WIL>
A;Molecule type: DNA
A;Residues: 1-1171 <WIL>
A;Cross-references: EMBL:AL117195; PIDN:CAB55018.1; CESP:Y57A10A.m
A;Experimental source: clone Y57A10A
C;Genetics:
A;Genetics:
A;Affer: CESP:Y57A10A.m

; 0 Gaps .; Query Match 51.2%; Score 43; DB 2; Length 1171; Best Local Similarity 66.7%; Pred. No. 79; Astches 8; Conservative 2; Mismatches 2; Indels N

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arginine-tRNA ligase (EC 6.1.1.19) NWA1707 [imported] - Neisseria meningitidis (strain 27.5 pecies: Neisseria meningitidis (C.) Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 (C.) Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 (C.) Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 Arfitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:09JTM7; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493!
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyacces at materous merquence_revision at-mar-2000 #text_change 09-Jul-2004
Cyaccession: RelOTS
Rifethelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arginyl-tRNA synthetase NMB1506 [imported] - Neisseria meningitidis (strain MC58 serogrou C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-572 <TET>
A;Cross-references: UNIPROT:Q9JYM8; GB:AE002500; GB:AE002098; NID:g7226744; PIDN:AAF41862
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural zinc finger factor 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
54;
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ed. No. 54;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
50.0%; Score 42; DB
Best Local Similarity 61.5%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 61.5%; Score 42;
Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: argS; NMA1707
C,Superfamily: arginine-tRNA ligase
C,Keywords: ligase
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C;Superfamily: arginine-tRNA ligase
16
                                    | | | | | ::|:||
16 GTAVKMNRMPSSLSPP 31
1 GLAKKSKRNPANLTPP
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45 GAAKKAKQNPREL 57
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-572 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
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F81866
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C;Species: Arabidopsis thaliana ($\text{mouse-ear}$ cress)
C;Date: 16-\text{Ual-1999} #sequence_revision 16-\text{Ual-1999} #text_change 09-\text{Ual-2004}
C;Accession. T10652
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
A;Reference number: 216533
A;Accession: T10652
A;Molecule type: DNA
                                                                                                                                                                                                                                              Carbon catabolite repressor crel - fungus (Trichoderma harzianum)
N,Alternate names: glucose repressor crel
C;Species: Trichoderma harzianum
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
R;Ilmen, M.; Thrane, C.; Penttilae, M.
Mol. Gen. Genet. 251, 451-460, 1996
My;Iter The glucose repressor gene crel of Trichoderma: isolation and expression of a systemmen number: S70703, MUID:9628569; PMID:8709949
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A;Experimental source: cultivar Columbia; BAC clone T5F17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C)Genetics:
A,Gene: crel
C;Keywords: DNA binding; repressor; transcription regulation; zinc finger
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A;Map postition: 4.847.3; 328/3
A;Introns: 97/1; 243/3; 328/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 50.0%; Score 42; DB 2; Length 419; Best Local Similarity 50.0%; Pred. No. 39; Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-268,'S',270-409 <ILW>
A;Residues: EMBL:X95369; NID:g1177688; PID:g1177689
A;Experimental source: strain T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 42; DB 2;
57.1%; Pred. No. 38;
tive 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted to the EMBL Data Library, January 1996
A,Reference number: S73105
A,Accession: S73106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-409 <ILM1>
A;Cross-references: UNIPROT:Q99005; EMBL:X95369
A;Experimental source: strain T3
A;Accession: S77920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: mRNA
A, Residues: 1-409 < ILM2>
A, Cross-references: EMBL: X95369
A, Experimental source: strain T3
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262 AKRSRPNPPNSTAP 275
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Best Local Similarity 57.1<sup>5</sup>
Matches 8; Conservative
                                                                   :||||:||| | | 455 SKKSKKNPKNST 466
                                 3 AKKSKRNPANLT 14
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CyAccesion: D86193
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C., A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Aitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Feference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:09XXF3; EMBL:AL023838; PIDN:CAA19501.1; GSPDB:GN00022; CESP:3
A;Experimental source: clone Y43C5A
                                         A;Residues: 1-268 <SCH>
A;Cross-references: UNIPROT:P53701; EMBL:U36787; NID:g1209634; PIDN:AAB19007.1; PID:g120:
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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C,Superfamily: Arabidopsis thaliana hypothetical protein F5K20.160
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                                                                                                                                                                                                                                                                                    Length 268;
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                                                                                                                                                                                                                                                                           Score 41; DB 2;
Pred. No. 36;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 48.8%; Score 41; DB 2; Local Similarity 46.7%; Pred. No. 36; es 7; Conservative 5; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-269 <WIL>
                                                                                                                            A,Gene: GDB:HCCS; CCHL
A,Cross-references: GDB:636832; OMIM:300056
A,Map position: Xp22-Xp22-
C;Keywords: carbon-sulfur lyase; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riwhite, S. submitted to the EMBL Data Library, June 1998 A;Reference number: 220272 A;Accession: T26823
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                                                                                                                                                                                                                                                                                                                                                                                                                                          70 GTAAENKENLDPSNLMPP 87
                                                                                                                                                                                                                                                                                 48.8%;
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A;Introns: 9/3; 47/2; 85/2; 227/3
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Best Local Similarity 50.v.
Best Local Similarity 50.v.
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A;Molecule type: DNA
A;Residues: 1-280 <STC
               A; Molecule type: mRNA
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Best Local S:
Matches 7
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National Pages (Saconaromyces Cerevisiae)

C; Species: Saccharomyces cerevisiae

R; Bordonne, R; Camasses, A; Madania, A; Martin, R.P.; Poch, O.; Tarassov, I.A.; Minsc submitted to the Protein Sequence Database, July 1996

A; Reference number: S67034

A; Rocession: S67044

A; Rocession: S67044

A; Residues: 1-726 cabR.

A; Residues: 1-726 cabR.

A; Residues: Scarification S. Cerevisiae two-hybrid interactor with the C-terminus of Cdc12p.

A; Reference number: S59360

A; Accession: S59360

A; Accession: S59360

A; Accession: S59360

A; Accession: S9360

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.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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Pred. No. 1e+02;
1; Mismatches 4; Indels
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G02133
holocytochrome-c synthase (EC 4.4.1.17) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #te>
C;Accession: G02133
R;Schaefer, L.; Ballabio, A.; Zoghbi, H.Y.
R;Schaefer, L.; Ballabio, A.; Zoghbi, H.Y.
R;Schaefer, H.0824
A;Reference number: H00824
A;Reference number: H00824
A;Status: greliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
S67044
NFI1 protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLAKKS-KRNPANLTP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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nes 10; Conservative
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A,Grossranders: 1-022 calm.
A,Grossranders: Loughard; GB:AE004061; GB:AE003849; NID:99107747; PIDDN:AAF8534;
A,Experimental source: strain 9a5c
R,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A,Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.E., M.; Marques, E.C.; Myaki, C.Y.;
R.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; de Ollveira, R.C.; Palmieri, D.A.
A,Authors: ad Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira Silva, A.C.R.; da Silvaira, M.A.; da Silva, M.A.; da Silva, A.C.R.; da Silva, A.C.R.; da Silva, A.C.R.; da Silva, Silva, A.C.R.; da Silvaira Silva, A.C.R.; da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A,Reference number: A.S.S.S.
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyocin AP41 large chain - Pseudomonas aeruginosa transposon TnAP41
C;Species: Pseudomonas aeruginosa
C;Species: Os-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 830271; A47060; 827605
R;Sano, Y.; Kageyama, M.
Mol. Gen. Con. (Genet. 237, 161-170, 1993
A;Title: A novel transposon-like structure carries the genes for pyocin AP41, a Pseudomor A;Reference number: $30271; MUID:93204890; PMID:8384291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S30271
A;Molecule type: DNA
A;Residues: 1-777 <SAN>
A;Cross-references: UNIPROT:Q51502; GB:D12705; NID:g216903; PIDN:BAA02196.1; PID:g216904
R;Sano, Y.
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A;Title: The inherent DNase of pyocin AP41 causes breakdown of chromosomal DNA.
A;Reference number: A47060; MUID:93139066; PMID:8423163
A;Accession: A47060
B;Status: preliminary
A;Molecule type: protein
A;Rolecule: Cype: protein
C;Superfamily: pyocin AP41 large chain
C;Keywords: bacteriocin
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Pred. No. 1.1e+02;
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Pred. No. 88;
3; Mismatches
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Best Local Similarity
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C;Genetics:
A;Gene: XF2546
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                                                                                                                                                                                                                                                                                                                     hypothetical protein F5K20.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45926
R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23017
A;Accession: T45926
A;Status: preliminary
A;Acteus: Dreliminary
A;Acteus: Dreliminary
A;Residues: 1-281 <months
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C,Species: Archaeoglobus fulgidus
C,Species: Archaeoglobus fulgidus
C,Species: Archaeoglobus fulgidus
C,Species: Obec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C,Accession: H69363
R,Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J. Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Ayauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woses, C.R.; Venter, J.C.
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woses, C.R.; Venter, J.C.
A,Reference number: A69250; MuID:98049343; PMID:9389475
A,Accession: H69363
A,Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A,Residues: 1-565 «KLE»
A,Rocessiues: UNIPROT:029350; GB:AE001041; GB:AE00782; NID:92689364; PIDN:AAB9034
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C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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A;Introns: 194/2.
A;Note: FSK20.160
C;Superfamily: Arabidopsis thaliana hypothetical protein FSK20.160
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      Length 280;
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A,Experimental source: cultivar Columbia; BAC clone F5K20
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Pred. No. 38;
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48.8%; Score 41; DB 46.7%; Pred. No. 38; iive 4; Mismatches
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Matches 7; Conservative
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Q6101 cochliobolu
Aar29905 cochliobolu
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2086c9 dictyosteli
26buw6 debaryomyce
29vz30 drosophila
Aaf48000 drosophil
27z894 emericella
274770 nanoarchaeu
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071224 rhodopirell

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Copyright (c) 1993 - 2004 Compugen Ltd
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1: uniprot_sprot:*
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Aas12031 treponema
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09jym8 neisseria m
09jym8 homo sapien
09cyz7 rattus norv
09cw51 tracophila
Aaf4098 drosophila
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:BACGCSE.1 (Novel protein similar to human procadherin 15 (PCDH15))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name_BAC7CSB.1;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Ocprinidae; Danio.
NCBI_TaxID=7955;
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SEQUENCE FROM N.A.
Liloyd D.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
-1-SIMILARITY: Contains 4 cadherin domains.
EMBL; AL592062; CAD52120.1; -
RSP; PIS116; INGT.
GO; GO:0015020; F:calcium ion binding; IEA.
GO; GO:00156; P:calcium ion binding; IEA.
R GO; GO:00156; P:calcium ion binding; IEA.
R GO; GO:00156; P:calcium ion binding; IEA.
R GO; GO:00156; Cadherin.
R FEan; PR00215; Cadherin.
R FRANT; SM00112; CA, 5.
R PROSITE; PS00228; CADHERIN. 1; 2.
R PROSITE; PS00228; CADHERIN. 1; 2.
R PROSITE; PS00228; CADHERIN. 2; 4.
Calcium; Calcium-binding.
NON TER
CAS AA; 69282 MW; 70EC5EZDOFBCFC3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.0%; Score 47; DB 2; Length 623; 60.0%; Pred. No. 39; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to KLAOD161159 Kluyveromyces lactis IPF 4333.1.
ORFNames=YALI0F05126g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      623
69282 MW; 70ECSE2DOF8CFC3A CRC64;
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                 0702T0
077010
097013
093044
AAS12031
SYR NEIMA
SYR NEIMB
081HR3
096PY4
096PY4
096PY4
096PY4
AAP49098
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Best Local Similarity 60.0
Matches 9; Conservative
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 277
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54.8%;
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184 AKKKKTPTTTPP 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 5/...
Best Local Similarity 5/...
                                                                                               Conservative
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                                                                                                                                                      3 AKKSKRNPANLIPP
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                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 10895;
PubMed=15001715;
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AAS51116;
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Q7VB38
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Mal., Muller H.,
Nicaud J.M., Nikolski M., Ozzier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Micker P., Soulet J.L.;
Micker P., Soulet J.L.;
Micker P., Soulet J.L.;
Micker P., Soulet J.L.;
Micker S., Marker S., Mesolowski M., Westhof E., Wirth B.,
Genome evolution in yeasts.";
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Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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NCBI_TaxID=33169;
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Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a tool for mapping the ancient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG77826.1; -.
SEQUENCE 716 AA; 76068 MW; 614189D84C66C243 CRC64;
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InterPro; IPR001950; TIF_SUI1.
Pfam; PF01253; SUI1; 1.
TIGRFAMS; TIGRO1159; DRP1; 1.
SEQUENCE: 1995 AA; 22543 MW; 02433AB5F7F94F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Science 304:304-307(2004).
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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174 QTHRSPANLTPP 185
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STRAIN=ATCC 10895;
Pubmed=15001715;
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STRAIN=CLIB99;
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Name=ACL112C;
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MEDLINE-SARG / CCMP 1375 / SS120;

MEDLINE-SARG / CCMP 1375 / SS120;

MEDLINE-SARG / CCMP 1397 / SA120;

Burbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,

Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,

Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,

Molf Y.I., Hess W.R.;

"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,

"Tannarly minimal oxyphototrophic genome.";

"Andi Y.I., Adad. Sci. U.S.A. 100:10020-10025 (2003).

EMBL; AE017164; AAQ00306.1; -.

ROG, GO:0016740; F:transferase activity; IEA.

RICEPRO, IPR002656; Acyl_transf_3.
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                                                          Gaps
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EMBL, ALO16886; AAS5116.1; - SEQUENCE 199 AA; 22543 MW; 02433ABSF7F94F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae, Eremothecium
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  Length 199;
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                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
predicted membrane associated acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashbya gossypii (Yeast) (Eremothecium gossypii).
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Pred. No. 17;
  5;
                                                                                                                                                                                                                                                                                                     199 AA
Score 46; DB Pred. No. 17;
                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                        PRT;
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Query Match

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S KW DR

OGSLC1 OGSLC1 RESULT 6 Q6SLC1 ID Q6SL

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STRAIN=C4;
Pubmed=14665450;
Catlett N.L., Yoder O.C., Turgeon B.G.;
"Whole-genome analysis of two-component signal transduction genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Aecomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                 Cochliobolus heterostrophus (Drechslera maydis).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.6%; Score 45; DB 2; Length 1943; 50.0%; Pred. No. 3e+02; Live 3; Mismatches 5; Indels
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BOYEr J., Fairhead C., Gaillon L., Galisson F., Michaux G., Thierry A., Dujon B.;
Submitted (UTL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal pathogens.";
Bukaryotic cell 2:1151-1161(2003).
EMBL; AY45029: AAA29905.1; -
SEQUENCE 1943 AA; 212673 MW; 8F8485E22FFC3A45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
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EMBL; Z75146; CAA99459.1; -.
PIR; 867131; 867131.
SGD; 800057434 677338.
GO; GO:0005737; C:cytoplasm; IDA.
SEQUENCE 306 AA; 35591 MW; 6CA44EED5C9D7E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
S. cerevistae chromosome XV reading frame ORF YOR238w
ORFNames=YOR238W;
                                                                                                 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Putative response regulator receiver RIMISp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 AA.
                                           PRT; 1943 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 GLAEQSATDPGNCAPP 233
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                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                           AAR29905
AAR29905;
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Q86KC9
ID Q86K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C4;
PubMed=14665450;
CabMed=14665450;
Whole-genome analysis of two-component signal transduction genes in "Whole-genome analysis of two-component signal transduction genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal pathogens.";

Eukaryotic Cell 2:1151-1161(2003).

Eukaryotic Cell 2:1151-1161(2003).

EMBL, AV456C93, AAR29050.1, ...

EMBL, AV456C93, AAR29050.1, ...

EMBL, AV456C93, AAR29050.1, ...

EnterPro; IPR011006; Chev_like.

R InterPro; IPR0010019; Kinase_like.

InterPro; IPR000019; Prot Kinase.

R InterPro; IPR000199; Prot Kinase.

R InterPro; IPR000199; Response_reg.

InterPro; IPR001290; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PR00069; PR1088; 1.

R Pfam; PR00069; PR1088; 1.

R Pfam; PR00019; Prot Kinase; 2.

R Pfam; PR00199; Response_reg; 1.

R Probom; P0000019; Prot Kinase; 2.

R R SMART; SM01219; TyrK; 1.

R R RART; SM01219; TyrK; 1.

R R RART; SM0119; PROTEIN KINASE DOM; 1.

R R ROSITE; PS00110; RESPONSE REGULATORY; 1.

R R ROSITE; PS00110; RESPONSE REGULATORY; 1.

R R ROSITE; PS00110; RESPONSE REGULATION; Sensory transduction; Serine/threenine-protein kinase; Transferase.

C SEQUENCE 1943 AA; 212673 MW; 8F8485E22FFC3A45 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cochliobolus heterostrophus (Drechslera maydis).
Eukaryota: Fungi, Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
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50.0%; Pred. No. 3e+02;
ive 3; Mismatches 5; Indels
                                                                                                                                                                                  Score 45; DB 2; Length 696;
Pred. No. 97;
0; Mismatches 4; Indels
InterPro, IPR006025, Pept M Zn BS.
Pfam; PF01757, Acyl transf 3; 1
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
Acyltransferase; Complete protecome; Transferase
SEQUENCE 696 AA; 79572 MW; 628FP962C9072747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Putative response regulator receiver RIMISp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1943 AA
                                                                                                                                                                                      53.6%;
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                                                                                                                                                                                                                                                                                                          1 GLAKKSKRNPANL 13
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                               Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuvegliee C., Talla E.,

A Goffard N., Frangeul L., Ahgle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich Juh., Beyne E., Blackasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Josep P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lemaire M., Mal., Muller H.,

Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,

Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Wincker P., Souciet J.L.;

"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                          Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome E of STATION CBS767 of Debaryomyces hansenii.
0RFNames=DEHA0E194049,
0RFNames=DEHA0E194049,
Eukaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryomyces hansenii (Yeast) (Torulaspora hansenii).
Saccharomycetales, Saccharomycetaceae; Debaryomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart C;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AC1169556; AAO51128.1;
InterPro, IPR008615; FNIP.
Pfam; PF05725; FNIP.
Hypothetical protein.
SEQUENCE 453 AA, 51421 MW; 5C79A3D45C13B1CD CRC64;
                                                                                                              Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium. Nobi_TaxID=44689;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        MEDLINE=22092622; PubMed=12097910;
                                                                                                           Hypothetical protein.
Dictyostelium discoideum (Slime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNEKSLKNPLNIYPP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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STRAIN=CBS767;

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RAY MEDLINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., RA George R.A., Lewis S.E., Flands S., Ashburaner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburaner M., Henderson S.N., Ratton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X., Printer B.D., RA Brandon R.C., Baladin D., RA Brandon R.C., Baladin D., RA Balaew R.M., Baut A., Bardell M.D., Baryakataroghu L., Bealey E.B.D., RA Ballew R.M., Banco P.V., Berman B.P., Bhandari D., Bolahakov S., Ballew R.M., Bacon K.Y., Benco P.V., Berman B.P., Bhandari D., Bolahakov S., Bortier P., Borthis P., Brothist P., Bonck J., Bew L., Dist S., Gars M.S., Gelbart H.M., Glasser K., Anderson R., Bough S., Dounkow B.C., Dunn P., Bratis N.L., Harvey D., Heiman T.G., Hernandez J.R., Pleusk W., Anderson B.L., Harvey D., Heiman T.G., Weiller S., Plants R.A., Houton K.A., Howland T.G., Weiller S., Rully D., Lia Z., Lina Y., Mattei B., McIntoon T.C., Kravitz S., Kully D., Lia Z., Lina Y., Mattei B., McIntoon T.C., Marshy D., McIntoon D., Mattei B., McIntoon K.A., Li G., Morris O., Mosherson D., Ra, Reisen B., McIntoon K.A., Li G., Morris W. Woller S., Randing A.C., Standers R.D., Strong F., Gorner C., Truner R., Venter E., Wang X., Mattei B., McIntoon K., Naisskern D.R., Palazolo M., Strong R., Singh T., Randon D.R., Malaman G., Pan S., Pollard J., Wang X., Mattei B., McIntoon J., Strong R., Wollessenbach J., Wang X., Wassarman D.A., Weinstock G., Zhu S., Zhu S.,
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                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroides, Drosophilidae, Drosophila.
                                                                                  Length 688;
                                                                                    52.4%; Score 44; DB 2; Length 686
66.7%; Pred. No. 1.4e+02;
.ive 3; Mismatches 1; Indels
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382137; CAG88371.1; -.
SEQUENCE 688 AA; 77169 MW; 23B2BBBB3F07BBD71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     (TremBlrel. 13, Created)
(TremBlrel. 16, Last sequence update)
(TremBlrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                            PRT; 3539 AA.
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                                                                                                                                                                                                                   272 LSKRIKKNPANL 283
                                                                                                           Local Similarity 66.7
nes 8; Conservative
                                                                                                                                                                            2 LAKKSKRNPANL 13
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=CG11122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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01-MAR-2001
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                                                                                         Query Match
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RAY MEDLINE=20196006; PubMed=10731132;

RAMAME M.D., Celniker S.E., Holf R.A., Broskins R.A., Galle R.F.,

RAMEM M.D., Celniker S.E., Hilp P.W., Hoskins R.A., Galle R.F.,

RAMEM M.D., Celniker S.E., Hilp P.W., Hoskins R.A., Galle R.F.,

RAME M.D., Celniker S.E., Richards S., Ashburner M. Henderson S.N.,

RAME Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RAME M. Hosyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

RAME Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RAME Beson K.Y., Benos P.V., Berman B.P., Branderio C.R., Cabor G.L.,

RAME Beson K.Y., Benos P.V., Berman B.P., Branderio L., Beasley B.M.,

Ballew R.M., Basu A., Baxendale J., Bayarktaroglu L., Beasley B.M.,

RAMELIS K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RAMELS K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RAME Cherry J.M., Candy S., Dahlke C., Davenport L.B., Davies P.,

RAME Cherry J.M., Candy F. Gorrell J.H., Gu Z., Galbart W. M. Glasser K.,

RAME R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RAME R.J., Gong F. Gorrell J.H., Gu Z., Galbart W. M. Glasser K.,

RAMELS K.J., Gabriellan A.E., Gart, R.S., Mul D. J.A., Keechum K.A.,

Alali M., Kalush F., Kalpen G.H., Ke Z., Kull D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Mei M.H., Ibegwam C.,

RAMEL R. Mount S.M., Moy W. Murphy B., Murphy L., Morphersin J.,

RAMEL R. Mount S.M., Moy W. Murphy B., Murphy D.M., Nelson D.L.,

RAMES D. M. Pittman G.S., Pan S., Pollard J., Puri V., Rees M.G.,

RAMES D. M. Rahing A.C., Pan S., Pollard J., Puri V., Resen M.G.,

RAMES D. M. Rahing A.C., Ramos I., Simpson M., Stupski M.P., Smith H.O.,

RAMES D. R. Mount S.M., Weinscon M., Stupski M.P., Smith H.O.,

RAMES D. R. Mount S.M., Weinscon M., Stupski M.P., Smith H.O.,

RAMES D. R. Mount S.W., Woodager W., Weinsenbach J.,

RAMES D. R. Mount S.W., Woodager W., Weinsenbach J.,

RAMES D. M., Wood R. W., Weinscholm W., Stups S., Sun E.,

RAMES D. Mount S.W., Woodsger W., Weinscholm W., Stups S., Sun E.,

      George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacieb U.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22446070; PubMed=12537573;
MEDLINE=22446070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Mistage S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Raminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,

Battencourt B.R., Celniker S.B., de Grey A.D., prysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.4%; Score 44; DB 2; Length 3539;
53.3%; Pred. No. 8.46+02;
ive 3; Mismatches 4; Indels
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EMBL; AB003485; AAF48000.3; -
Flybase; PBgn0030266; CGIII12.
GO; GO:0005654; C:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
Interro; IPRO0086; zf-C2H2; 3.
EAMRT; SM00355; ZnF C2H2; 5.
FROSITE; PS00028; ZINC_FINGER_C2H2 1; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2 2; 3.
SEQUENCE 3539 AA, 384995 MW; 0BD4A2997D18E0CI CRC64;
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7; 0BD4A2997D18E0C1 CRC64;
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                                                                                                                                                                                                                                                                                                Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Best Local Similarity 53.30,
Best Local Similarity 53.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12.M., Kronmiller B., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paciffer B.D., Richards S., Sodergren E.J., Weinskas R., Tabor P.E., Wan K., Stapheton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Prinshing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=22426069; PubMed=12537572;
Mistra B., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Amainker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J. Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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"Annotation of the Drosophila melanogaster euchromatic genome:
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UT 01-APR-2004 (TrEMBLrel. 27, Created)
DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-APR-2004 (TrEMBLrel. 27, Last sequence update)
DF 01-APR-2004 (TrEMBLrel. 27, Last annotation update)
DF CG11122-PA.
GG11122-PA.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
X NCBI TaxID=7227;
VEBI TaxID=7227;

RESULT 12
AAF48000
ID AAF48000
DT 01-A

167 AA

Created) PRT;

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PRELIMINARY;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                               NCBI_TaxID=160232;
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, Emericella.
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Pred. No. 1.2e+03;
2; Mismatches 4; Indels
                                                                                                                                                          Length 3539;
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EMBL; AE003485; AAF48000.3; -.
FlyBase, FBGN0030266; CGIII 22.
SEQUENCE 3539 AA, 384994 MW; 0BD4A2997D18E0C1 CRC64;
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PS00012; PHOSPHOPANTETHEINE; UNKNOWN 1.
4793 AA; 525432 MW; DD4186E99190B601 CRC64;
                                              to the EMBL/GenBank/DDBJ databases
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                         Score 44; DB 2; 1
Pred. No. 8.4e+02;
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002)
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Local Similarity 53.3%;
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Submitted (SEP-2002)
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Name=sidC;
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Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).

BMBL, AB017199, ARR38927.1; -. Complete protecome.

Complete protecome.
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STRAIN=Kin4-M;

MEDLINE=22946215; PubMed=14566062;

MEDLINE=22946215; PubMed=14566062;

Beeson K.Y., Hibbs L., Bolanos R., Keller M., Kretz K., Lin X.,

Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,

Soell D., Stetter K.O., Short J.M., Noorderwier M.,

"The genome of Nanoarchaeum equitans: Insights into early archaeal
evolution and derived parasitism.";

Proc. Natl. Acad. SGI, U.S.A. 100:12984-12988(2003).

ERBL, AB017199; ARRS9271.; -.

SEQUENCE 167 AA; 20126 MW; CCB6FDJDE0EA7483 CRC64;
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Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 4
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Archaea; Nanoarchaeota; Nanoarchaeum
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Search completed: November 10, 2004, 13:38:44

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MADLE dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - western lowland gorilla mitochond MADH2 dehydrogenase (ubiquinone oxidoreductase chain 1 c)species: mitochondrion Gorilla gorilla gorilla (western lowland gorilla) (c)accession: A59153 (c)accession: A59153 (c) Accession: A59153 (c
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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96 64.9 322 96 64.9 322 94 63.8 334 92 62.2 322 92 62.2 322 92 62.2 322 92 62.2 322 91 61.5 322 91 61.5 322 90 60.8 324 90 60 60 60 80 80 90 60 80 80 80 90 80 80 80 80 90 80 80 80 80 90 80 80 80 80 80 80 90 80	NADH2 dehydrogenas 116 NADH2 dehydrogenas 890 NADH2 dehydrogenas 820 NADH2 dehydrogenas 820 NADH2 dehydrogenas 892 NADH2 dehydrogenas 892 NADH2 dehydrogenas 893 NADH2 dehydrogenas 853 NADH2 dehydrogenas 854 NADH2 dehydrogenas 857 NADH2 dehydrogenas 857 NADH2 dehydrogenas 854 NADH2 dehydrogenas 857 NADH2 dehydrogenas 867 NADH2 dehydrogenas 867 NADH2 dehydrogenas 8687 NADH2 dehydrogenas 8687 NADH2 dehydrogenas 8687 NADH2 dehydrogenas 8698 NADH2 dehydrogenas 8600 NADH2 dehydrogenas	e) (EC 1.6.5.3) chain 1 - human mitochondrion none oxidoreductase chain 1 sapiens (man) care (man) 23-Oct-1981 #text_change 09-Jul-2004 Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin,	f the human mitochondrial genome. 73052; PMID:7219534 GB:J01415; GB:M12548; GB:M58503; GB:M63932; GB:M6393	oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t) tted complex; mitochondrion; NAD; oxidative phosphorylation; c 5.5%; Score 131; DB 1; Length 318; 7.3%; Pred; No. 1.2e-10; 7.3%; Pred; No. 1.2e-10; 8.7%; Pred; No. 1.2e-10; 9.7%; Pred; Pred
10 96 64.9 322 2 2 3 3 3 4 5 2 2 3 3 4 6 3 5 3 3 4 5 2 2 3 3 4 6 3 5 3 3 4 5 2 2 3 2 2 3 2 2 3 2 2 3 2 2 3 2 3 2 2 3 3 2 2 3 3 3 2 2 3 3 3 2 3	868128 111181010 11118100 11118100 1111810 1111810 1111810 1111810 1111810 1111810 1111810 1111810 1111810 1111810 1111810 11810 11810	(EC 1. ne oxid piens (vision arrell,	on of t:811730 86; GB:	oreduct complex Score Pred. 2; Mi
11 96 64.9 322 12 94 63.5 334 13 94 63.5 334 14 92 62.2 323 15 92 62.2 323 16 92 62.2 323 16 92 62.2 323 17 92 61.2 323 18 91 61.5 323 19 60.8 324 10 91 60.8 324 11 90 60.8 324 12 90 60.8 324 13 90 60.8 324 14 90 60.8 324 15 90 60.8 324 16 90 60.8 324 17 1 17 1 18 90 60.8 324 18 90 60.8 324 19 60.8 324 19 60.8 324 19 60.8 324 19 60.8 324 10 60.8 324 11 90 60.8 324 12 90 60.8 324 13 90 60.8 324 14 90 60.8 324 15 90 60.8 324 16 80.8 324 17 1 18 90 60.8 324 18 90 60.8 324 19 60.8 324 19 60.8 324 10 60.8 324 10 60.8 324 11 90 60.8 324 12 90 60.8 324 13 90 60.8 324 14 90 60.8 324 15 90 60.8 324 16 90 60.8 324 17 10 60.8 324 18 90 60.8 32	0000000000000000	reas .	ati UID 038	Ха С В В В В В В В В В В В В В В В В В В В
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11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			77-465, 19 mnce and o mmber: A00 000407 000407 318 (AND> mnces: UNI: NDI mnces: GDB mnces: GBB mnces: GBB mnces: GBB mnces: GBB mnces: GBB mnces: GBB	MADH:qui embrane-as. similarity conser!
- General Contract Co		RESULT 1 NADH2 dehydrog N.Alternate na C.Species: mit C.Pate: 22-May C.Accession: A C.Adcession: A	Nature 290, 45 A,Title: Seque A,Reference nu A,Reference nu A,Molecule Lyp A,Residues: 1- A,Crosi-refere C,Genetics: R,Genetics A,Gene: GDB: MA A,Cross-refere A,Map position A,Genetic mitc	Superfamily: Keywords: me Query Match Best Local S Matches 28

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Gaps

Pred. No.

76.7%;

C;Genetics:

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C,Accession: T11363
R;Xu, X.; Gullberg, A.; Arnason, U.
Nol. Evol. 43, 438-463, 1996
A;Title: The complete mitchondrial (mtDNA) of the donkey and mtDNA comparisons among for A;Reference number: Z17265; MUID:97032591; PMID:8875857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: mitochondrion
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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C; Species: mitochondrion Equus caballus (domestic horse)
C; Date: 16-Ual-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: T11857
R; Xu, X.; Arnason, U
R; Xu, X.; Arnason, U
R; Xi, 198, 357-367, 1994
R; Xi-198, 357-367, 1994
R; Xi-198, 357-367
R; Xi-198, 357-367
R; Xi-198, 357-367
R; Xi-198, 350-367
R; Xi-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-318 <XUX>
A;Residues: UNIPROT: P92475; EMBL: X97337; NID: g1805746; PIDN: CAA66014.1; PID: g180
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C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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C;Genetics:
A;Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                            NADHZ dehydrogenase (ubiquinone) (EC 1.6.5:3) chain 1 - donkey mitochondrion C;Species: mitochondrion Equus asinus (donkey)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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Pred. No. 3.4e-07;
6; Mismatches 3; Indels
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9.46-08;
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                                                                                                                                                                                      2 NILLLIMVPILIAMAFLMLTERKILGYIQPR 31
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70.0%;
                                                               23; Conservative
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Matches 21; Conservative
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                       Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
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T11857
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T11247
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C.bate: 02-Apr-1982 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C.batecssion: A00409
R.Bibb, M.J.; Van Etten, R.A.; Wright, C.T.; Walberg, M.W.; Clayton, D.A.
C.batecssion: A00409
A.fitle: Sequence and gene organization of mouse mitochondrial DNA.
A.Ritle: Sequence and Gene organization of mouse mitochondrial DNA.
A.Residus: 1-315 ABB>
A.Rocession: A00409
A.Molecule type: DNA
A.Residues: 1-315 ABB>
A.Rocession: MUSPROT:P03888; GB:J01420; NID:G3342520; PIDN:AAB486641; PID:G9895295
A.Note: the authors translated the initiation codon ATT for residue 1 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T11833
R,Arnason, U.; Gullberg, A.; Xu, X.
Herditas 124, 185-189; 1996
A,Title: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar
A,Reference number: 217353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Genome: mitochondrion
A;Genetic code: SGC1
A;Note: NADH:
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A,Genetic code: SGCI
A,Start code: SGCI
A,Start conde: ATT
C,Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                   A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: NAPH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
T11833
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common gibbon mitochondrion
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Cross-references: UNIPROT:Q96126; EMBL:X99256; PIDN:CAA67628.1
Experimental source: isolate Ester
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Pred. No. 1e-08;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         Length 318;
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                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                         Score 131; DB 2;
Pred. No. 1.2e-10;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
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I Similarity 83.3%;
25; Conservative
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Best Local Similarity 90.3%;
Matches 28; Conservative
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Best Local Similarity
                                                                   A; Gene: NADH1
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A;Genome: mitochondrion
A;Genetic code: SGC4
A;Genetic code: SGC4
C;Supert codon: GTG
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; C
                                                                                                                                                                                                                                                             Score 104; DB 2;
Pred. No. 6.2e-07;
5; Mismatches 4;
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Best Local Similarity 70.0%;
Matches 21; Conservative
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A58888
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - rabbit mitochondrion (fragment)
C;Species: mitochondrion Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: 111480
R;Gissi, C; Gullberg, A; Arnason, U.
Genomics 50, 161-169, 1998
A;Title: The complete mitochondrial DNA sequence of the rabbit, Oryctolagus cuniculus.
A;Reference number: Z17275; MUID:98317530; PMID:9653643
A;Accession: T11480
A;Accession: T11480
A;Accession: T11480
A;Residues: 1-318 <GIS>
A;Residues: I-318 <GIS>
A;Cosses-references: UNIPROT:079427; EMBL:AJ001588; NID:g3293006; PIDN:CAA04847.1; PID:g3
A;Genetics:
C;Genetics:
A;Genetic code: SGCI
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
R;Xu, X.; Janke, A.; Arnason, U.
Mol. Biol. Bvol. 13, 1167-1173, 1996
Mol. Biol. Bvol. 13, 1167-1173, 1996
A;Title: The complete mitochondrial DNA sequence of the greater indian rhinocerus, Rhind
A;Reference number: Z17256; MUID:97051708; PMID:8896369
A;Reference number: Z17256; MUID:97051708; PMID:8896369
A;Accession: T11247
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-318 <XUX>
A;Cross-references: UNIPROT:096189; EMBL:X97336; NID:g1666193; PIDN:CAA66001.1; PID:g166
A;Residues: mitochondrion
A;Genome: mitochondrion
A;Genome: mitochondrion
C;Genome: mitochondrion
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit I/[NiFe]-hydrogenase-3-C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 552972
G;Accession: 552972
A;Trozater, R.H.; Crozater, Y.C.
Genetics 13, 97-117, 1993
A;Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence and A;Reference number: 552960; MUD:93114603; PMID:8417993
A;Accession: 552972
A;Accession: 552972
A;Residues: 1-305 <CRO>
A;Residues: 1-305 
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70.9%; Score 105; DB 2;
Best Local Similarity 70.0%; Pred. No. 4.7e-07;
Matches 21; Conservative 5; Mismatches 4.
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A;Cross-references: UniPROT: P03887; GB:J01394; NID:g336430; PIDN:AAB59268.1; PID:g336431; B;Yagi, T.; Hatefi, Y.
Biol. Chem: 263, 16150-16155, 1988
Biol. Chem: 263, 16150-16155, 1988
A;Title: Identification of the dicyclohexylcarbodiimide-binding subunit of NADH-ubiquinor A;Title: Identification of the dicyclohexylcarbodiimide-binding subunit of NADH-ubiquinor A;Reference number: A31910; MUID:89034077; PMID:3141400
A;Reference number: A31910
A;Residues: 1-15 < YAG>
C;Genetics: 1-15 < YAG>
C;Genetics: Code: SGCI
C;Superfamily: NADH: quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-ty
C;Keywords: blocked amino end; membrane-associated complex; mitochondrion; NAD; oxidative
F;1/Modified site: N-formylmethionine #status experimental
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A,Status: nucleic acid sequence not shown; translation not shown; not compared with concet
A,Molecule type: DNA
A,Residues: 1-318 <JAN>
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Cjate: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
Cjacession: A58888
Rjacke, A.; Gemmell, N.J.; Feldmaier-Fuchs, G.; von Haeseler, A.; Paabo, S.
Mol. Byol. 42, 153-159, 1996
A;Title: The mitochondrial genome of a monotreme--the platypus (Ornithorhynchus anatinus A;Reference number: A58888; MUID:97077300; PMID:8919867
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G;Accession: A00408; A31910  
A;Accession: A00408  
A;Tile: Complete sequence of bovine mitochondrial DNA. Conserved features of the majorent complete sequence of bovine mitochondrial DNA. Conserved features of the majoresion: A00408  
A;Accession: A00408  
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A, Genome: mitochondrion
A, Genetic code: SGC1
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A;Cross-references: UNIPROT:079874; EMBL:AF034253; NID:g4958951; PID:g4958952; PIDN:AAD34 R;Ursing, B.M.
R;Ursing, B.M.
A;Description: The EMBL Data Library, February 1999
A;Description: The complete mitochondrial DNA sequence of the pig (Sus scrofa).
A;Reference number: Z17370
A;Accession: T11870
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                                                                                                                                                     P.C.; Mao, S.J.T.; Hua
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A,Genteic code: SGG1
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-ty
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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A,Gentaio ode: SGC1
C,Superfamily: NADH:guinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t)
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c
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Modecule type: DNA
A;Residues: 1-323 «GDE»
A;Cross_references: UNIPROT:P03890; GB:M10217; GB:X01600; GB:X01601; GB:X02890; NID:9343
         NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - pig mitochondrion C;Species: mitochondrion Sus scrofa domestica (domestic pig) (C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 09-Uul-2004 C;Accession: T10972; T11870 R;Lin, C.S.; Liu, C.Y.; Sun, Y.L.; Chang, L.C.; Cheng, I.C.; Yang, P.C.; Mao, S.; Submitted to the EMBL Data Library, November 1997 A;Pescription: Complete nucleotide sequence of the porcine mitochondrial genome. A;Reference number: Z17237
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A,Molecule type: DNA
A,Residues: 1-55, F' 57-63, A, 65-77, A', 79-318 <URS>
A,Cross-references: EMBL:AJ002189; PIDN:CAA05229.1
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Pred. No. 2.3e-06;
5; Mismatches 5;
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illarity 66.7%;
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Matches 20; Conserv
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C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A.Genne: mitochondrion
A.Genetic code: SGCI
C.Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C.Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C.Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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Til428

What is a second to be considered by the complete mitochondrion of Species: mitochondrion Macropus robustus (wallaroo, euro)
C;Species: mitochondrion Macropus robustus (wallaroo, euro)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Til428
R;Janke, A.; Xu, X.; Arnason, U.
Proc. Natl. Acad. Sci. U.S.A. 94, 1276-1281, 1997
A;Title: The complete mitochondrial genome of the wallaroo (Macropus robustus) and the Reference number: 217271; MUID:97188458; PMID:9037043
A;Reference number: 217271; MUID:97188458; PMID:9037043
A;Reference by complete mitochondrial genome of the wallaroo (Macropus robustus) and the Reference number: 217271; MUID:97188458; PMID:9037043
A;Reference number: 217271; MUID:97188458; PMID:9037043
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                                                                                       Score 104; DB 2; Length 318;
Pred. No. 6.4e-07;
7; Mismatches 3; Indels
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7; Mismatches 4; Indels
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Best Local Similarity 63.3%;
Matches 19; Conservative
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Best Local Similarity 70.0%;
Matches 21; Conservative
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Best Local Similarity 66.7
Matches 20; Conservative
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A; Note: NADH1 C; Superfamily: C; Keywords: men

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RESULT 14

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Homo sapiens (Human).
Mitochondarion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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STRAIN=MagnasanM.N.320HgC;
Starikovskaya E.B., Sukernik R.I., Derbeneve O.A., Volodko N.V.,
Ruiz-Pesini E., Torroni A., Brown M.D., Lott M.T., Hosseini S.H.,
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AAT37866;
01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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Aac17866 homo sapi
O85kt1 homo sapien
O87kt1 homo sapien
O6704 homo sapien
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O67042 homo sapien
O67712 homo sapien
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O67710 homo sapien
O77044 homo sapien
O77044 homo sapien
O77049 homo sapien
O77041 homo sapien
O85kus homo sapien
                                                                                                                                               November 10, 2004, 12:27:34; Search time 37.8532 Seconds (without alignments) 471.205 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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148.
1 ANLLLIMVPILIAMAFLMLTERKILGYIQPR 31
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Q8hhh3 home sapien Q94920 gorilla gor Q9b115 home sapien Q9b104 home sapien Q9b2v3 home sapien Q9b2x4 home sapien Q9b2x5 home sapien Q8wcx2 home sapien A154410 home sapi Aa154410 home sapi Aa154423 home sapi				Euteleostomi; ; Homo.	L., Zhang YP.; inferred from	C64; ngth 318;	
08HHH3 09T20 09T20 09BLL5 09BLN4 09BZV7 09BZX5 09BZX5 08WCX2 AALS4184 AALS410 AALS4410 AALS4410	ALIGNMENTS	PRT; 318 AA.	Created) Last sequence update) Last annotation update)	Craniata, Vertebrata, Catarrhini, Hominidae	delt HJ., Zhu C rial DNA lineages).	CE7B297 CR DB 2; Le .9e-09; es 1;	1 ANLLLLMVPILIAMAFLMLTERKILGYIOPR 31
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Matches

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TISSUE=Placenta;
MEDLINE=95132634; PubMed=7530363;
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Homo sapiens (Human).
Mitochondrion.
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BMC Genet. 2:13-13(2001).
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Best Local Similarity
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21-JUL-1986 (Rel
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MEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MEDLINE=22406325; PubMed=12509511;
MEDLINE S. METALOR M. M. Essley K., Chen E., Brown M.D.,
A Sukernik R.I., Olckers A., Wallace D.C.; Brown M.D.,
A Sukernik R.I., Olckers A., Wallace D.C.;
MEDLIA ALVIS A. 100:177-176 (2003)
MELLIA ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
MEDLIA AV195783; AAO89774-1;
MITCEPPOR AV19784; MADRIA AV19785-1;
MITCEPPOR AV19784; MADRIA AV19784; AANBERDOREZDE845 CRC64;
MITCEPPOR AV19784; MATANA AV19784; MATAN
Huoponen K., Wallace D.C.;
"Mitochondrial DNA diversity in indigenous populations of southern extent Siberia, and the origins of native american haplogroups.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYG15359; AAT17866.1; -.
Mitochondrion.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UAR-2003 (TrEMBLrel. 24, Last annotation update)
NADH dehydrogenase subunit 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 1.
                                                                                                                                                                                                                                                                                                            Score 133; DB 2;
Pred. No. 1.9e-09;
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Mitochondrion.
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Q85KT1
AC Q85KT1,
DT O1-JUN-10
DT O1-JUN-10
DE NADH del
DE NADH CAPA
OC BURDAN
OC CO -1- SIM
OC CO -1- CAT
OC CO -1- CAT
OC CO -1- CAT
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DR GMBL; AM
DR GMBL; AM
DR GMG, GO:
DR GMG
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RESULT 4

ð g 28WCX9
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DT 011
DT 0

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Horai S., Hayasaka K., Kondo R., Tsugane K., Takahata N.;
"Recent African origin of modern humans revealed by complete sequences
of hominoid mitochondrial DNAs.";
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Pubmed=1294126; DOI=10.1093/molbev/msg230;
Moilanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in segment of MTND5 gene in haplogroup J.";
Mol. Biol. Evol. 20:2132-2142(2003).
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                           Maca-Meyer N., Gonzalez A.M., Larruga J.M., Flores C., Cabrera V.M., "Major genomic mitochondrial lineages delineate early human
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=81173052; PubMed=7219534;
Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
Coulson A.R., Drouin J., Eperon I.C., Nietlich D.P., Roe B.A.,
Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.,
"Sequence and organization of the human mitochondrial genome.";
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PROSITE; PS00668; COMPLEXI_NDI_2; 1.
Mitochondrion; NAD; Oxdoreductase; Transmembrane; Ubiquinone.
SEQUENCE 316 AA; 35432 MW; 0258880098F7D7BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 316;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3)
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Ingman M., Gyllensten U.; "Mitochondrial genome variation and evolutionary history of Australian
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PubMed=14766490; DOI=10.1007/$00414-004-0427-6;
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irwin J.A., Parsons T.J.;
"Single mucleotide polymorphisms over the entire mtDNA genome that
increase the power of foreasic testing in Caucasians.";
Int. J. Legal Med. 118:137-146(2004).
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Howell N., Kubacka I., Xu M., McCullough D.A.;
"Leber hereditary optic neuropathy: involvement of the mitochondrial
ND1 gene and evidence for an intragenic suppressor mutation.";
Am. J. Hum. Genet. 48:935-942(1991).
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Ingman M., Kaessmann H., Paabo S., Gyllensten U.;
"Mitochondrial genome variation and the origin of modern humans.";
Nature 408:708-713(2000)
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MEDLINE=92026096; PubMed=1928099;
Mebell N., Bindoff L. A., McCullough D.A., Kubacka I., Poulton J.,
Mackey D., Taylor L., Turnbull D.M.;
"Leber hereditary optic neuropathy: identification of the same
mitochondrial NDI mutation in six pedigrees.";
Am. J. Hum. Genet. 49:939-950(1991).
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MEDLINESA1107577; PubMed=6260957;
Sanger F., Coulson A.R., Barrell B.G., Smith A.J.H., Roe B.A.,
"Cloning in single-stranded bacteriophage as an aid to rapid DNA
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MEDLINE-92070510; PubMed=1959619;
Majander A., Huoponen K., Savontaus M.-L., Nikoskelainen E.,
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22723755; PubMed=12840039; DOI=10.1101/gr.686603;
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MEDLINE=91241131; PubMed=1674640;
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MEDLINE=91144615; PubMed=1900003;
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Genome Res. 13:1600-1606(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 314:592-597(1985).
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A Thew MILOCODOMIZED LDNA MULGALION ASSOCIATION WALL, MONITORDOMIZED LDNA MULGALION ASSOCIATION WALL, MONITORION ASSOCIATION WALL, MONITORION ASSOCIATION ASSOCIAT
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                                                                                                                                                                                                                                                                    human mitochondrial DNA and translation products:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94010883; PubMed=8104867; Shoffner J.M., Brown M.D., Torroni A., Lott M.T., Cabell M.F., Mirra S.S., Beal M.F., Yang C.-C., Gearing M., Salvo R., Watte Juncos J.L., Hansen L.A., Crain B.J., Payad M., Reckord C.L.,
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Jaksch M., Hofmann S., Kaufhold P., Obermaier-Kusser B., Zierz
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"A new mitochondrial DNA mutation associated with non-insulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mitochondrial DNA variants observed in Alzheimer disease and Parkinson disease patients.";
[17]
                                                                                                                                        Marzuki S., Noez A.S., Lettrit P., Thyagarajan D., Kapsa R., Utthanaphol P., Byrne E.; Lettrit P., Thyagarajan D., Kapsa R., "Normal variants of human mitochondrial DNA and translation probe building of a reference data base."; Hum. Genet. 88:139-145(1991).
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-1- SIMILARITY: Belongs to the complex I subunit 1 family.
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[14]
VARIANTS PRO-205; CYS-255 AND PRO-288.
MEDLINE-92098084; PubMed=1757091;
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MEDLINE=95251666; PubMed=7733935;
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Fri Nov 12 14:55:08 2004

EMBL; EMBL;

EMBL; EMBL; EMBL; EMBL;

Matches

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88.5%; Score 131; DB 2; Length 318;

Query Match

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No. 1910

SEQUENCE FROM N.A.

Pubmed=14760490;

Challed M.D. Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Chole M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

Challed M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

A. Chole M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

R. Irwin J.A., Parsons T.J.;

Tricease the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-02004;

Int. J. Legal Med. 0:0-02004;

C. -! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. -! CATALYTIC ACTIVITY: NADH + ubiquinone.

BENBL, AV495134; AAR93068:1, ---

C. -! SIMILIARITY: Belongs to the complex I subunit 1 family.

ROG: G0:0005739; C:mitochondrion; IEA.

InterPro; PRO01669; NADHGA; I.

PROSITE: P800669; COMPLEXI NDI 1; 1.

PROSITE: P800669; COMPLEXI NDI 1; 1.

PROSITE: P800669; COMPLEXI NDI 1; 1.

R.Mitochondrion; NAD: Oxidoreduciase; Transmembrane; Ubiquinone.

SW Mitochondrion; NAD: Oxidoreduciase; Transmembrane; Ubiquinone.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

A Startkovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,

A Startkovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,

A Huoponen K., Wallace D.C.;

Huoponen K., Wallace D.C.;

Huoponen K., Wallace D.C.;

Tetent of Siberia, and the Origins of Native American Haplogroups.";

Ann. Hum. Genet. 0:-0(2004)

C. -! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. -! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C. -! SIMILARITY: Belongs to the complex I subunit I family.

RMBL; AYS19488; AAR31258.1, -

RRBL; AYS19488; AAR31258.1, -

RRBL; AYS19488; AAR31258.1, -

RRBL; ARS1125 PRO01694; RSP_NADH_dhl.

PROSTITE: PSO0667; COMPLEXI. ND1 1; 1.

PROSTITE: PSO06667; COMPLEXI. ND1 1; 1.

PROSTITE: PSO0666; COMPLEXI. ND1 1; 1.

PROSTITE: PSO0666; COMPLEXI. ND1 2; 1.

PROSTITE: PSO06667; COMPLEXI. ND1 2; 1.

PROSTITE: PSO0667; COMPLEXI. ND1 2; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Micochondrion.
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
NS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                       NADH dehydrogenase subunit 1.
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Query Match
Best Local Similarity 90.33,
Best Local 28, Conservative
                                                                                                                             Homo sapiens (Human).
Mitochondrion.
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Starikovskaya E.B., Sukernik R.I., Derbeneva O.A., Volodko N.V.,
Torroni A., Ruiz-Pesini E., Brown M.D., Lott M.T., Hosseini S.H.,
Torroni A., Wallace D.C.;
"Mitochondrial Dan Diversity in Indigenous Populations of Southern
Extent of Siberia, and the Origins of Native American Haplogroups.";
Ann. Hum. Genet. 0.0-0[204].
-- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-- SIMILARITY: Belongs to the complex I subunit 1 family.
EMBL, AYS19490; AAR91284.2, --
GO; GO:0005739; C:mitochondrion; IEA.
Interpro; IRR001684; Resp_NADH_dhl.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 3.6e-09;
2; Mismatches 1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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1 Similarity 90.3%;
28; Conservative
                                                                                                            AAP89114.1;
AAP89127.1;
AAP89140.1;
                                                                                                                                                                                                                                                                                                                                           AAP89244.1;
AAP89257.1;
                                                                                                                                                                                                                                                                                                  AAP89218.1;
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                                             AAP89075.1;
                                                                                                                                                                                AAP89153.1;
AAP89166.1;
                                                                                         AAP89101.1;
                                                                 AAP89088.1;
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Best Local Similarity 90.33
Matches 28; Conservative
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Mitochondrion.
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Best Local Similarity
                                                                                                                                                             AY339410;
                                                                                                                                                                                   AY339411;
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                                             AY339405;
                                                                                           AY339407;
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                                                                   AY339406
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QGROUG

RESULT 6
96R006
1D 06R01
DT 06-U
DT 05-U
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Gaps

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Length 318;

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EMBL; AY495125; AAR92551.1; -. EMBL; AY495125; AAR92551.1; -. GO, GO:005739; C:mitochondrion; IEA.
GO, GO:005739; C:mitochondrion; IEA.
InterPro; IPRO0169; Resp.NADH_dhl.
PROSITE; PSO0667; COMPLEXI ND1 1; 1.
PROSITE; PSO0668; COMPLEXI ND1 2; 1.
Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone. SEQUENCE 318 AA; 35690 MW; 2F6F93D304893D18 CRC64;
                                                                                                                                                              Query Match 88.5%; Score 131; DB 2; Length 31 Best Local Similarity 90.3%; Pred. No. 3.6e-09; Matches 28; Conservative 2; Mismatches 1; Indels
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Best Local Similarity 90.35
Matches 28; Conservative
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Q6VH72
ID Q6VH72
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QERRM1
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Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,
Irvin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
-!- CATALYITC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Belongs to the complex I subunit I family.
EMBL, AY495131; AAR93029.1; -.
GO; GO:0005739; C:mitochondrian; IEA.
InterPro; IPRO01694; Resp_NADH_dhl.
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-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                      Gaps
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Mitochondriton.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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PROSITE; PS00667; COMPLEX1, ND1 1; 1.
PROSITE; PS00668; COMPLEX1, ND1 2; 1.
Mitochondrion; NAD: Oxidoreductase; Transmembrane; Ubiquinone.
SEQUENCE 318 AA; 35690 MW; D483BICS61AB2F31 CRC64;
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                    Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
     90.3%; Pred. No. 3.6e-09;
tive 2; Mismatches 1;
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                                                  1 ANLLLLMVPILIAMAFLMLTERKILGYIOPR 31
                                                                     4 ANLLLLIVPILIAMAFLMLTERKILGYMQLR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
     Best Local Similarity 90.3
Matches 28; Conservative
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                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                Mitochondrion.
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QGRR93;
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206RR39
206RR39
AC 066RR39
DT 05-UI
DE NABH
RA ITWILL
RA ITWILL
RA ITWILL
RA ITWILL
CC -I-C
CC -I-C
CC -I-C
DR EMBL
DR FEM
DR PROS;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PSOU667; COMPLEXI ND. 2; 1.
PROSITE; PSOU668; COMPLEXI ND. 2; 1.
Mitochondrion; NAD, Oxidoreductaes; Transmembrane; Ubiquinone. SEQUENCE 318 AA; 35660 MW; 2EC48962B4892D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 318;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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90.3%; Pred. No. 3.6e-09;
live 2; Mismatches 1
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                                        1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
                                                              4 ANLLLLIVPILIAMAFLMLTBRKILGYMQLR 34
                                                                                                                                                                                        318 AA
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Fri Nov 12 14:55:08 2004

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X PubMed=12949165.

X PubMed=12949165.

A Moilanen J.S., Finala S., Majamaa K.;

T. Lineage-specific selection in human mtDNA: lack of polymorphisms in a segment of MTNDS gene in haplogroup J.";

Mol. Biol. Evol. 20:2133-2142(2003).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-!- SIMILARITY: Belongs to the complex I subunit 1 family.

EMBL; AX139545; AA99085.1; --

R GO; GO:0005739; C:mitochondrion; IEA.

R FEBL; AX139545; AA99085.1; --

R GO; GO:0005739; C:mitochondrion; IEA.

R PROSITE; PS00667; COMPLEXI.NDI.1; 1.

R PROSITE; PS00668; COMPLEXI.NDI.1; 1.

R PROSITE; PS00668; COMPLEXI.NDI.1; 1.

R PROSITE; PS00668; COMPLEXI.NDI.2; 1.

R Mitochondrion; NAD; Oxidoreductaes; Transmembrane; Ubiquinone.

SEQUENCE 318 AA; 35618 MW; 721B7AD6F96539FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mitochondrial DNA transit between West Asia and North Africa inferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maca-Meyer N., Gonzalez A.M., Pestano J., Flores C., Larruga J.M.,
Cabrera V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.5%; Score 131; DB 2; 90.3%; Pred. No. 3.6e-09; iive 2; Mismatches 1
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90.3%; Pred. No. 3.6e-09;
iive 2; Mismatches 1;
Finnila S., Lehtonen M.S., Majamaa K.; "Phylogenetic network for European mtDNA."; Am. J. Hum. Genet. 68:1475-1484(2001).
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Best Local Similarity 90.5.,
Best Local Similarity 20.5.,
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Mitochondrion.
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PubMed=14563219;
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Q6WQ94;
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A Trwin J.A., Farsons T.J.;

A Trwin J.A., Barsons T.J.;

I Increase the power of forensic testing in Caucasians.";

I Int. J. Legal Med. 0:0-0(2004).

C -! - CAPALYIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C -! - CAPALYIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

C -! - SIMILARITY: Balongs to the complex I subunit 1 family.

EMBL; AV33559; AAP91467.1; -.

REMBL; AV495209; AAR9404.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Catarrhini; Hominidae; Homo.
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PROSITE; PS00667; COMPLEXI ND1 2; 1.
PROSITE; PS00668; COMPLEXI ND1 2; 1.
SEQUENCE ND10 NND; COMPLEXI ND1 2; 1.
SEQUENCE 318 A.M. 35664 NW, 0895BFRGC65002FA6 CRC64;
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                                          05.UUL-2004 (TrEMBLrel. 27, Created)
05.UUL-2004 (TrEMBLrel. 27, Last sequence update)
05.UUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.5%; Score 131; DB 2; L 90.3%; Pred. No. 3.6e-09; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonen M.S., Majamaa K.;
"Phylogenetic network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANLLLLMVPILIAMAFLMLTERKILGYIQPR 31
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SEQUENCE FROM N.A.
MEDLINE=21313109; PubMed=11349229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADH dehydrogenase subunit 1.
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Mitochondrion.
                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12949126;
                                                                                                                                                                                                                                            Mitochondrion.
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QEVIFO;
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                                                                                                                                                                                Name=ND
              Q6VH72;
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Search completed: November 10, 2004, 13:38:23 Job time : 38.8532 secs

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Sequence 17, Appl Sequence 463, Appl Sequence 21689, Appl Sequence 25834, Appl Sequence 547, Appl Sequence 5747, Appl Sequence 14, Appl Sequence 11, Appl Se
                                                                                                                   November 10, 2004, 12:32:37; Search time 10.3627 Seconds (without alignments) 191.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
1: /cgT2_6/ptodata1/iaa/5A_COMB.pep:*
2: /cgT2_6/ptodata1/iaa/5B_COMB.pep:*
4: /cgT2_6/ptodata1/iaa/6A_COMB.pep:*
5: /cgT2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgT2_6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/ptodata1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-583-110-4693

US-09-248-796A-21089

US-09-248-796A-21089

US-09-248-796A-21089

US-09-248-796A-25834

US-09-248-796A-26751

US-09-248-796A-26751

US-09-248-796A-26751

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US-08-18-19-18

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US-08-19-18-18

US-08-140-721A-18

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US-08-140-721A-18

US-08-140-721A-18

US-08-619-790C-18

US-08-619-790C-18

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US-08-619-790C-18

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150
1 LRLNITVWPTIITPILLTLFLITNRLITTR 30
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Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                    protein
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RESULT 1
US-09-097-889-17
US-09-097-889-17
Sequence 17, Application US/09097889
Petent No. 621817
GENERAL INFORMATION:
APPLICANT: Herristad, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: ACMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRATE: Washington
COUNTRY: USA
ZIP: 98104
117, Appl
15, Appl
15, Appl
17, Appl
17, Appl
17, Appl
17, Appl
18, Appl
18, Appl
18, Appl
18, Appl
133, Appl
133, Appl
133, Appl
133, Appl
133, Appl
137, Appl
137, Appl
137, Appl
10, Appl
10, Appl
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98104
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSENMEN Ph.D., Stephen J.
REFERENCE/DOCKET NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acids
TYPE: ALLIAND ACCORDED TO THE COMPANIED TO THE CO
                     US-08-095-068-15
US-08-095-068-17
US-08-140-721A-15
US-08-140-721A-15
US-08-140-721A-15
US-08-619-790C-17
US-07-785-565A-17
US-07-785-565A-17
US-09-098-079-18
US-09-097-899-18
US-09-499-039-12035
US-09-499-039-12035
US-09-499-039-12035
US-09-569-68-37
US-09-569-68-37
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Best Local Similarity 69.0%; Pred. No. 7.4e-07;
Matches 20; Conservative 6; Mismatches 2
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TOPOLOGY: linear
US-09-097-889-17
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Sequence 25834, Application US/09248796A

Sequence 25834, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 25834
                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-09-248-796A-21089

J Sequence 21089, Application US/09248796A

J Sequence 21089, Application US/09248796A

J Sequence 21089

J Sequence 21089

J Sequence 21089

J Sequence 21089, Application US/09248796A

J SETTLE NOT THE SETTLE WEIGHTON: FOR DIAGNOSTICS AND THERAPEUTICS

J TILE SETTLENCE 107196.132

J CURRENT APPLICATION NUMBER: US/09/248,796A

J CURRENT PILING DATE: 1998-02-13

J PRIOR PILING DATE: 1988-02-13

J PRIOR PILING DATE: 1988-08-13

J PRIOR PILING DATE: 1998-08-13

J NUMBER OF SEQ ID NOS: 28208

J SEQ ID NO 21089
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                                                                                                                                     Length 440;
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10;
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14;
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                                                                                                                                  Score 54; DB
Pred. No. 14;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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                                         TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 UMPTIITPILLITLELITUR 25
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52 LWLLLIPIFLTIFLIARR 70
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                                                                                                                                     36.0%;
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Best Local Similarity 47.4%;
Matches 9; Conservative ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Candida albicans
US-09-248-796A-21089
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                                                                                                                                     Query Match
Best Local Similarity 40.6
Matches 13; Conservative
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US-09-248-796A-25834
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                                                                                        US-09-583-110-4693
SEQ ID NO 4693
LENGTH: 440
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ORGANISM:
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Beten No. 6699703

GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANTON: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-707
CURRENT FILING DATE: US 09/107,433
PRIOR APPLICANTON NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR PLING DATE: 1998-06-30
PRIOR PRILING DATE: 1998-06-30
PRIOR PRILING DATE: 1998-06-30
PRIOR PILING DATE: 1997-07-02
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                                                                          Sequence 17, Application US/09098079
Sequence 17, Application US/09098079
Sequence 17, Application US/09098079
Select No. 6489095
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Paris, Roin F.
TILE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.3%; Score 102.5; DB 4; Length 68; 69.0%; Pred. No. 7.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WHER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RENTTVWPTIITPILLTLFLITN-RLITT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REPERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 68 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.03
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                Above
STREET: 6300
CITY: Seattle
The Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-09-583-110-4693
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-098-079-17
                                                                     US-09-098-079-17
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Sequence 26751, Application US/09248796A

Sequence 26751, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR PELING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

LENGTH: 60

LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8270, Application US/09543681A

Patent No. 6605709

Patent No. 6605709

TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT PILING DATE: 1999-04-05

PRIOR PILING DATE: 1999-04-09

SEQ ID NO 8270

LENGTH: 302
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                                                                                                                                                                                                                                                                                                                                                                                                                  37 RRNPSMWMPLMIHQLRSHQVPLLIHPLWLTCYRVTNRRI 75
                                                                                                                                                                                                                                                                                                                                                                                      ---PTITPILLTLFLITNRLI
                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                         Ouery Match
34.3%; Score 51.5; D
Best Local Similarity 30.8%; Pred. No. 31;
Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42198
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ TOWARE: PatentIn Ver. 2.0
SEQ ID NO 42198
LENGTH: 456
                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LKTTLTPTLVVPILVT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Candida albicans
US-09-248-796A-26751
                                                                                                                                                                                                                                                                                                                                                                                      2 RLNTTVW-----
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                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                       Sequence 547, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICAMT: Griffais, R.

ATTILE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering REPRENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REPERSENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 57472

LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parent No. -6703491
GENERAL INFORMATION:
APPLICANT: Hondrich et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.7%; Score 52; DB 4; Length 286; Best Local Similarity 50.0%; Pred. No. 16; Atches 13; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | ::| | ::| | 37 RRNPSMWMPLMIHQLRSHQVPLLIHPLWLTCYRVTNRRI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PTITPILLTLFLITNRLI
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Pred. No. 18;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-57472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 1...286
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LCLKQTKWSPIISPIKAFLYLFVVTN 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LRLNTTVWPTIITPI--LLTLFLITN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
209-270-767-57472
: Sequence 57472, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42198, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
74 LWLLLIPIFLTIFLIARR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.8%;
Matches 12; Conservative
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US-09-270-767-42198
                                                                                                RESULT 6
US-09-198-452A-547
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34.0%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13

(US-08-055-917-16

) Sequence 16, Application US/08055917

) Patent No. 5310875

) GENERAL INFORMATION:

APPLICANT: Chang, Tse Wen; Chang, Nancy T.

ITLE OF INVENTION: Peptides corresponding to membrane-bound 1gA, NUBER OF SEQUENCES: 19

CORRESPONDENCE: Tanox Biosystems, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 65;
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                                                                                                                                                                                    Score 49; DB 1;
Pred. No. 9.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.7%; Score 49; DB 1
64.7%; Pred. No. 9.2;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,120
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
NAME: Mirabel, Eric P.
REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TIX89-04CCC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FEDDABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Tanox Biosystems, Inc. 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-055-917-18
;.Sequence 18, Application US/08055917
                                                                                                                                                                                                                             2;
             TELEFAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (713) 664-2288
TELEFAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VWPTIITPILLTLFLIT 23
                                                                                                                                                                                                                                                                                                                 27 impirir--Firiris 41
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                                                                                                                                                                                      Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 65 amino acids
TYPE: amino acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
32.77
Best Local Similarity 64.77
Matches 11; Conservative
                                                                      co amino co

TOPOLOGY: Linear

US-08-055-917-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
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CITY: HOLL
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-055-917-16
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APPLICANT: Kelth Weinetock et al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

ITILE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196.13

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-13

PRIOR PELING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20246
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Patent NO. 5310875
GENERAL INFORMATION:
APPLICANT: Chang, TSE WEN; Chang, Nancy T.
ATTLE OF INVENTION: Peptides corresponding to membrane-bound IgA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tanox Blosystems, Inc.
STREET: 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
33.3%; Score 50; DB 4; Length 129;
Best Local Similarity 47.6%; Pred. No. 14;
Matches 10; Conservative 6; Mismatches 5; Indels
                    11; Indels
Best Local Similarity 48.1%; Pred. No. 24;
Matches 13; Conservative 3; Mismatches
                                                               1 LRLNTTVWPTIITPILLTLFLITNRLI 27
                                                                                                    39 LREGETVYRWALIPLILLFLILGSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TNX89-04CCC IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Texas
COUNTRY: USA
ZIP: 77025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NUMBER: US/08/055,917
                                                                                                                                                                                                        Seguence 20246, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,120
FILING DATE: 11/4/1991
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1983
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LNTTVWPTIITPILLTLFLIT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ISTTMKLSSVTPLLLTLLFT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mirabel, Eric P. REGISTRATION NUMBER: 3
                                                                                                                                                                                             US-09-248-796A-20246
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2; Gaps
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Pred. No. 9.2;
                                                  FILING DATE: 9/16/1901
APPLICATION NUMBER: 07/455,080
FILING DATE: 12/22/1989
ATTORNEY/AGENT INFORMATION:
NAME: Mirabel, Eric P.
REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TNX89-04DEE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 664-228
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 10, 2004, 13:44:01 Job time : 10.3627 secs
M DATA:
07/760,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 VWPTIITPILLTLFLIT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 LWPTTIT--FLTLFLIS
          PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-095-068-14
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Sequence 14 Application US/08095068

Fatent No. 5362643

GENERAL INFORMATION:
APPLICANT Chang, TSE Wen; Chang, Nancy T.
TITLE OF INVENTION: an immunogen
TITLE OF INVENTION: an immunogen
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tanox Biosystems, Inc.
STREET: 10301 Stella Link Rd.
CITY: Houston
STREET: 10301 Stella Link Rd.
CITY: Houston
STREET: 10501 Stella Link Rd.
COUNTEX: USA
TITLE OF DISPESS:
ADDRESSEE: Tanox Biosystems, Inc.
STREET: 10501 Stella Link Rd.
COUNTEX: USA
STREET: USA STEET
COMPUTER: USA STELLATION DATA:
FILING DATE:
                          APPLICANT: Chang, Tse Wen; Chang, Nancy T.

TITE OF INVENTION: Peptides corresponding to membrane-bound 1gA

TITE OF INVENTION: Peptides corresponding to membrane-bound 1gA

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tanox Biosystems, Inc.

STREET: 10301 Stella Link Rd.

CITY: Houston

STATE: Pexas

COUNTRY: USA

ZIP: 77025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION S30
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/45,080
FILING DATE: 11/4/191
APPLICATION NUMBER: 07/45,080
FILING DATE: 11/4/191
APPLICATION NUMBER: 31,211
REPERENCE MUMBER: 31,211
REPERENCE POWER: 31,211
REPERENCE POWER: 31,211
REPERENCE CONTINUED OF SEQUENCE TELECOMMINICATION: 17ELEPAN: (713) 664-2894
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.7%; Score 49; 55.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/055,917
                                                                                                                                                                                                                                                     ZIP: 77025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::||| :| |||:
26 SLWPTTVT--FLTLFLIS 41
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-055-917-18
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US-08-095-068-14
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Sequence 337725, Sequence 169176, Sequence 169176, Sequence 5361, App Sequence 2397, App Sequence 2997, App Sequence 276546, Sequence 276546, Sequence 2134, App Sequence 25, App 1 Sequence 18, App Sequence 126321, Sequence 21662, Sequence 281162, Sequence 281261, Sequence 281261, Sequence 281562, Sequence 28162, Sequence 281602, Sequence 136989, Sequence 133, App Sequence 133, App

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Sequence 27, Appl
Sequence 17, Appl
Sequence 139, Appl
Sequence 139, App
Sequence 25625,
Sequence 245, App
Sequence 245, App
Sequence 11334,
Sequence 11334,
Sequence 159528,
Sequence 159528,
Sequence 159528,
Sequence 15831,
                                                                                      November 10, 2004, 16:36:12; Search time 32.228 Seconds (without alignments) 328.807 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1. /cgn2_6/ptodata/1/pubpaa/Der_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/Der_PUBMP PUBL.pep:*
3. /cgn2_6/ptodata/1/pubpaa/Der_PUBMP PUBL.pep:*
4. /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
7. /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13. /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 US-10-092-750-27

US-10-264-049-4146

US-10-264-049-4146

US-10-408-765A-139

6 US-10-408-765A-139

7 US-10-425-115-256252

5 US-10-424-776-245

5 US-10-474-776-245

6 US-10-474-599-187835

6 US-10-474-776-245

7 US-10-369-493-15813

4 US-10-369-493-16212
                                                                                                                                             US-10-092-750-27
150
1 LRLNTTVWPTIITPILLTLFLITNRLITTR 30
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           1566620 segs, 353225886 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                Minimum DB 8
Maximum DB 8
                                                                   protein
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                                                                                          Run on:
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ALIGNMENTS

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Sequence 27, Application US/10092750

1S-10-022-750-27

Sequence 27, Application US/10092750

Publication No. US2003003157A1

GENERAL INPORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alphin, Julia

TITLE OF INVENTION: POLYPEPTIGES Interactive with BCL-X1

TITLE OF INVENTION: POLYPEPTIGES INCOME.

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT APPLICATION NUMBER: US/60/274,526

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOUTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO. 27

LENTH: 30

LENTH: 30
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100.0%; Score 150; DB 14;
Best Local Similarity 100.0%; Pred. No: 2.4e-13;
Matches 30; Conservative 0; Mismatches 0;
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US-10-264-049-4146
Sequence 4146, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-750-27
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Best Local Similarity 69.0%; Pred. No. 1.6e-06;
Matches 20; Conservative 6; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
65.7%; Score 98.5; DB 16; Length 68;
Best Local Similarity 65.5%; Pred. No. 5.6e-06;
Matches 19; Conservative 6; Mismatches 3; Indels
                Length 68;
                                                                                                                                                                                                                                                                                                      APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
APPLICANT: Giben, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Bary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERSENCE: 660088-465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                        Indels
              Score 102.5; DB 9;
Pred. No. 1.6e-06;
6; Mismatches 2;
                                                                                             2 RENTTVWPTIITPILLTLFLITN-RLITT 29
                                                                                                                     3 QLNTTVWPTMITPMLLTLFLITQLKMLNT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RINTIVMPTIITPILLILELITN-RLITT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 OLNTTVWPIMITPMLLTLFLITQLKMLNT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-408-765A-1491
; Sequence 1491, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                            RESULT 4
US-10-408-765A-139
US-10-408-139, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
applICANT: Fahy, Edin D.
                    68.3%;
  Query Match
Best Local Similarity 69.0.
Best Local Similarity 69.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                ; LOCATION: (55) ; COTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pahy, Eoin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: 225
                                                                                                                                                                                                                                                                                                                                                                                                   Score 103.5; DB 15; Length 65;
Pred. No. 1.1e-06;
3; Mismatches 2; Indels 1;
HAPPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAl331
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/2669
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 NITVWPTIITPILLTLFLITN-RLITT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTTVWPTITPILLTLFLITQLKILNT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09098079 Patent No. US20020064773A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8%;
Matches 21; Conservative 3
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_PEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
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US-09-098-079-17
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  Gaps
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APPLICANT: Zhang, Bing
APPLICANT: Gleno, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
TATLE OF INVENTION: TRAGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10011161 S.
CURRENT FILING DATE: 2003-04-04
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 1491
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RESULT 8
US-10-474-776-245
US-10-474-776-245
Sequence 245, Application US/10474776
Publication No. US20040110181A1
GENERAL INFORMATION:
JAPPLICANT: WYETH
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYPE
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
TITLE OF INVENTION: MUMBER: US/10/474,776
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 245
LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9

US-10-424-599-159528

US-10-424-599-159528

SUBJICATION NO. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21($5322) 803-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENGINE OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
FEATURE:
COMMENDATION: Clone ID: PAT_MRT3847_115073C.1.pep
US-10-424-599-159528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.0%; Score 54; DB 16; Best Local Similarity 40.6%; Pred. No. 43; Matches 13; Conservative 7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.3%; Score 53; DB 15; Best Local Similarity 50.0%; Pred. No. 10; Matches 9; Conservative 5; Mismatches 4
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae US-10-474-776-245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bathazuk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LRLNTTVWPTIITPILLT 18
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US-10-437-963-111334
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                                                                                                                                RESULT 6
105-105-256252
15 Sequence 256252, Application US/10425115
16 Publication No. US20040214272A1
16 GENERAL INFORMATION:
17 APPLICANT: La Rosa, Thomas J.
18 APPLICANT: Cao, Yinua
18 APPLICANT: Cao, Yongwei
19 APPLICANT: Cao, Yongwei
10 APPLICANT: Cao, Yongwei
10 APPLICANT: APPLICANT: Cao, Yongwei
10 APPLICANT: Cao, Yongwei
10 APPLICANT: Cao, Yongwei
10 APPLICANT: Cao, Yongwei
11 TITLE OF INVENTION: Noleic Acid Molecules and Other Molecules Associated With
11 TITLE OF INVENTION: Noleic Acid Molecules and Other Molecules Associated With
12 TITLE OF INVENTION: NONERR: 2003-04-28
12 CURRENT APPLICATION NOMBER: 2003-04-28
13 NUMBER OF SEQ ID NOS: 369326
14 SEG ID NO 256252
15 LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Show Yihua
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187835
LENGTH: 75
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40.3%; Score 60.5; DB 17; Length 86;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 14; Conservative 0; Mismatches 6; Indels 1
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US-10-424-599-187835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Clone ID: MRT4577_165293C.1.pep
US-10-425-115-256252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (1)..(86)
OTHER INFORWATION: unsure at all Xaa locations
FEATURE:
                                  3 QLNTIVWPTMITPMFLTLFLITQLKMLNT 31
        2 RINTTVWPTIITPILLTLFLITN-RLITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 187835, Application US/10424599 ; Publication No. US20040031072A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 NIXVWPXIXFPITXLXLFLIT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 NTTVWPTIITPI-LLTLFLIT 23
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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US-10-424-599-187835
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Gaps

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Indels

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Xiandeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURE OF SECURITY SE
                                                                                                                                                                                                                                                                                                                    DB 14; Length 430;
57;
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57;
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                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                Score 53;
Pred. No. 5
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Pred. No. 5
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; Sequence 16212, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                          TYPE: PRT ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT CARANISM: Xanthomonas campestris
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Best Local Similarity 40.0%;
Matches 10; Conservative 6
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Best Local Similarity 40.0%;
                          NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15831
LENGTH: 430
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ORGANISM: Zea mays
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Sequence 156.2 Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Chec, Yongwei

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 15462
TITLE OF INVENTION: Rice Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15831, Application US/10369493

Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_15321C.1.pep
US-10-437-963-111334
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35.3%; Score 53; DB
Best Local Similarity 40.0%; Pred. No. 57;
Matches 10; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 LPTTHWPTIITTMAVLLSILSSSFL 278
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ORGANISM: Xanthomonas campestris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 40.03
Matches 10; Conservative
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ORGANISM: Oryza sativa
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Gaps

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34.7%; Score 52; DB 17; Length 43;

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RESULT 15
US-10-289-762-547
US-10-289-762-547
Sequence 547, Application US/10289762
Sequence 547, Application US/10289762
Sequence 547, Application US/00606218A1
Sequence 547, Application US 00006218A1
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
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                                2; Gaps
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                                8; Indels
Best Local Similarity 50.0%; Pred. No. 7.4; Matches 14; Conservative 4; Mismatches
                                                                          4 NTTVWPTIITPILLTLFLI--TNRLITT 29
                                                                                                             11 NITHEPSILIPKPPTLFFIIPSNSTITT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 11, 2004, 01:28:09 Job time : 33.278 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
1.0CATTON: 1...286
1.OTHER INVERMATION: Xaa=unknown or other
1.0S-10-289-762-547
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November 10, 2004, 12:29:32; Search time 6.68394 Seconds (without alignments) 431.857 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                - protein search, using sw model
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                                                                                                                                               Run on:
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US-10-092-750-27 150 1 LRLNTTVWPTIITPILLTLFLITNRLITTR 30 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues Searched:

283416

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

SA	Description	H+-transporting tw	ᇊ	ᄆ	H+-transporting tw	ρυ	ng t	'NI e	v	hetical			₽	hypothetical prote	v		H+-transporting tw	H+-transporting tw	somal m	potassium efflux s	etical	tin		tin	g					
SUMMARIES		PWHU8	E59153	Ö	T14197	14	137051	14	33	T11510	AI1421	PWBO8	D97155	H95054	E97924	A99316	H98148	AD3139	T25180	F97738	137052	PWBO6	T11838	A54976	AE2777	B97557	14	_	35	97
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d	Query Match	8	4.	4.	4.	'n	ö	ű.	'n	œ.	۲.	e.	ů.	36.0	٠.	Ŋ.	ů.	ď.	'n.	4.	4	4.	4.	4.	4.	4.	ω,	m.	'n	ά.
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hypothetical prote	H+-transporting tw	ABC transporter, m	trehalose/maltose	conserved hypothet	hypothetical prote	H+-transporting tw	H+-transporting tw	H+-transporting tw	probable lprF prot	probable transport	membrane protein y	probable transport	Sodium, galactoside	flagellar biosynth	flagellar biogenes
H72557	PWHU6	AC2749	B97530	D89974	B70543	E58850	S41839	T11484	E70957	D85826	D64966	086065	AC0122	C81361	A49217
Ń	-	~	N	N	N	~1	N	N	N	~	N	~	N	~	N
181	226	305	305	325	446	63	67	67	261	352	352	352	477	724	724
32.7	32.7	32.7	32.7	32.7	32.3	32.0	32.0	32.0	32.0	32.0	32.0	32.0	32.0	32.0	32.0
		σ	49	6	'n	48	48	48	48	48	48	48	48	48	48
49	4	4	•	•	48										

ALIGNMENTS

RESULT 1 PWHUS
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - human mitochondrion N:Alternate names: hydrogen ion-transporting ATP synthase protein 8
C;Species: mitochondrion Homo sapiens (man)
.C;Date: 22-May-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A01062; 180237
R;Anderson, S.; Bankier, A.T.; Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin, i

Nature 290, 457-465, 1981

A; Title: Sequence and organization of the human mitochondrial genome.

A; Reference number: A00151; MUID:81173052; PMID:7219534

A; Accession: A01062

A; Molecule type: DNA
A; Residuces: 1-68 - ANDA; Cross-reference: UNIPROT: P03928; GB:J01415; GB:M12548; GB:M53932; GB:M63931
A; Residuces: 1-68 - ANDA; Cross-reference: UNIPROT: P03928; GB:J01415; GB:M12548; GB:M53932; GB:M63931
B; Horai, S.; Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Proc. Natl. Acad. Sci. U.S.A. 32. 532-536, 1995
A; Title: Recent African origin of modern humans revealed by complete sequences of hominon A; Reference number: 159384; MUID:95132634; PMID:7530363
A; Accession: 180237
A; Accession: 180237
A; Accession: 180237
A; Residuces: 1-31, 'S., 33-68 - RES>
A; Cross-references: GB:D38112; NID:9644480; PIDN:BAA07294.1; PID:9704445
C; Genetics:
A; Genetics:
A; Genetics: mitochondrion
A; Genetic code: SGC1
C; Superfamily: H+-transporting ATP synthase protein 8
C; Superfamily: H+-transporting ATP synthase protein
C; Keywords: ATP biosynthesis; -hydrolase; membrane-associated complex; mitochondrion; oxic

Gaps Match 68.3%; Score 102.5; DB 1; Length 68; Local Similarity 69.0%; Pred. No. 3.9e-07; es 20; Conservative 6; Mismatches 2; Indels

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2 RENTTVWPTITTPILLTLFLITN-RLITT 29 3 QLNTTVWPTMITPMLLTLFLITQLKMLNT 31 g ò

RESULT 2 E59153

H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - western lowland gorilla mitor NyAlternate names: hydrogen ion-transporting ATP synthase protein 8 C;Species: mitochondrion Gorilla gorilla gorilla (western lowland gorilla) C;Date: 03.Dec-1999 #sequence_revision 03.Dec-1999 #text_change 03.Jun-2002 C;Accession: E59153 R;Xu, X.; Arnason, U. Mol. Biol. Evol. 13, 691-698, 1996

Query Match 64.7%; Score 97; DB 2; Length 68; Best Local Similarity 81.8%; Pred. No. 2.2e-06; Matches 18; Conservative 3; Mismatches 1; Indels

A; Gene: ATPase8

g

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H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - pygmy chimpanzee mitochondric C;Species: mitochondrion Pan paniscus (pygmy chimpanzee, bonobo) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T14147
Froca. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995
A;Title: Recent African origin of modern humans revealed by complete sequences of hominoi A;Reference number: 159384; MuID:95132634; PMID:7530363
A;Accession: T1447
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-68 <HOR>
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C; Date: 31.MMay-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C; Date: 31.MMay-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
R; Horai, S.; Satta, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Taka A; Moll. 3, 32-43, 1992
A; Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.
A; Reference number: 137047; MUID:92389366; PMID:1518083
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A,Genteic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP blosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
C.Superfamily: H+-transporting ATP synthase protein 8
C.Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid
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A,Genteic code: SGC1
C,Superfamily: H+-transporting ATP synthase protein 8
C,Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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A,Molecule type: DNA
A,Residues: 1-68 4-08
A,Cross-references: UNIPROT:Q34801; GB:D38484; NID:g558513; PIDN:BAA07498.1; PID:g558518
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                                                                                             Length 68;
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                                                                                             Score 96; DB 2;
Pred. No. 3e-06;
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                                                                                             Query Match
Best Local Similarity 77.3%;
Matches 17; Conservative
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T14147
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T14024
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - gorilla mitochondrion C;Species: mitochondrion Gorilla gorilla (gorilla)
C;Species: mitochondrion Gorilla gorilla (gorilla)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14024
R;Horal, S: Hayasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Proc. Natl. Acad. Sci. U.S.A. 92, 532-536, 1995
A;Title: Recent African origin of modern humans revealed by complete sequences of hominc A;Reference number: IS9384; MUID:95132634; PMID:7530363
A;Accession: T14024
A;Accession: T14024
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-68 -HOR.
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A,Genetic code: SGC1
C,Superfamily: H+-transporting ATP synthase protein 8
C,Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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   A,Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla. A,Reference number: 217269; MUID:96212991; PMID:8676744
A,Recession: E59153
A,Status: preliminary; nucleic acid sequence not shown; translation not shown; translate A,Molecule type: DNA
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A)Genetic code: SGC1
C)Superfamily: H+-transporting ATP synthase protein 8
C)Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                             A;Cross-references: GB.X93347; NID:g1304307; GSPDB:GN00106
A;Cross-references: GB.X93347; November 1995
A;Note: this translation is not annotated in GenBank entry GGMITG, release 114.0
C;Genetics:
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Query Match 64.7%; Score 97; DB 2; Length 68; Best Local Similarity 81.8%; Pred. No. 2.2e-06; Matches 18; Conservative 3; Mismatches 1; Indels

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RESULT
RESULT 4

H-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - chimpanzee mitochondrion C;Species: mitochondrion Pan troglodytes (chimpanzee)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14197
R;Horal, S: Hayasaa, K.; Kondo, R.; Tsugane, K.; Takahata, N.
R;Horal, S: Hayasaa, K.; Kondo, R.; Tsugane, K.; Takahata, N.
A;Title: Recent African origin of modern humans revealed by complete sequences of homind A;Reference number: 159384; MID:95132634; PMID:7530363
A;Accession: T14197
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A;Molecule type: DNA
A;Residues: 1-68 <HOR>
A;Cress-references: UNIPROT:Q35647; EMBL:D38113; PIDN:BAA07300.1
C;Genetics: mitochondrion
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A Genome: mitochondrion
A Genetic SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A, Residues: 1-66 CAND>
A, Residues: 1-66 CAND>
A, Cross-references: UNIPROT: P03929; GB: J01394; NID: G336430; PIDN: AAB59272.1; PID: G336435;
R, Fearnley, I.M.; Walker, J.E.
B, Fearnley, I.M.; Walker, J.B6
A, Title: Two overlapping genes in bovine mitochondrial DNA encode membrane components of A, Reference number: A25474; MUID: 87004570; PMID: 2875870
                                                                  Cross-references: UNIPROT: Q9ZXYO; EMBL:Y18001; NID:g4049475; PIDN:CAA76998.1; PID:g4045
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S.Anderson, S.; de Bruin, M.H.L.; Coulson, A.R.; Eperon, I.C.; Sanger, F.; Young, J. Mol. Biol. 156, 683-717, 1982.
A,Title: Complete sequence of bovine mitochondrial DNA. Conserved features of the nA; Reference number: A00152; MUID:83010260; PMID:7120390
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 0.56;
5; Mismatches 5; Indels
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A,Molecule type: protein
A,Residues: 1-37;45-50;52-53 <FEA>
REWALKer, U.E.; Lutter, R.; Dupuis, A.; Runswick, M.J.
Biochemistry 30, 5369-5378, 1991
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Best Local Similarity 54.5%;
Matches 12; Conservative 9
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Best Local Similarity 48.0
Matches 12, Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-169 <GLA>
                         Residues: 1-68 <ARN>
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T14143

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - orangutan mitochondrion C.5pecial trochondrion Pongo pygmaeus (orangutan)
C.5pecial 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.7dcession: T14143
R.7Horal Agasaka, K.; Kondo, R.; Tsugane, K.; Takahata, N.
Proo. Natl. Acad. Sci. U.S.A. 92, 532-536
A;Title: Recent African origin of modern humans revealed by complete sequences of hominc A;Reference number: 159384; MUID:95132634; PMID:7530363
A;Reference number: 159384; MUID:95132634; PMID:7530363
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-68 -4DR>
A;Ross-references: UNIPROT:Q35584; EMBL:D38115; PIDN:BAA07309.1
C;Genetics:
A;Genemics: A;Genem
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T11837

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - common gibbon mitochondrion (5/5pecies: mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11837
R;Arnason, U; Gullberg, A; Xu, X.

Hereditas 124, 185-189, 1996
A;Title: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar A;Reference number: Z17353
A;Accession: T11837
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-68 cARN
C;Genetics: A;Residues: MylPROT:Q95705; EMBL:X99256; PIDN:CAA67632.1
A;Experimental source: isolate Ester
C;Genetics: A;Genetics: A;Genetics: A;Genetics: Code: SGCI
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tillio

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - baboon mitochondrion

G.Species mitochondrion Papio hamadryas (baboon)

C.Species mitochondrion Papio hamadryas (baboon)

C.Accession: Tillio

C.Accession: Tillio

M. Gullberg, A.; Janke, A.

J. Mol. Bvol. 47, 718-727, 1998

A;Ttle: Molecular timing of primate divergences as estimated by two non-primate calibra A;Reference number: Z17277; MUD:99065765; PMID:9847414

A;Accession: Tillio

A;Accession: 
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Pred. No. 0.00017;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RINTTVWPTITTPILLTLFLIT 23
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Best Local Similarity 72.7%;
Matches 16; Conservative
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nes 15; Conservative
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4

Score 54; DB 1; Length 66; Pred. No. 1.4; 6; Mismatches 5; Indels

Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative (

A, Molecule type: protein A, Residues: 1-5 <WAL> C, Genetics:

A; Genome: mitochondrion

2 RENTTVWPTIITPILLTLFLI 22 :|:|: | |:| : ||||:| QLDTSTWLTMILSMFLTLFII 23

ò Q RESULT 12

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Fighth, Confidence of the conf
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Richard D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc, P.; Sun, P.M.; Winkler, M.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc, J. Sun, P.M.; Winkler, M.; Zood
J.; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross_references: UNIPROT:Q8DQ23; GB:AE007317; PIDN:AAK99225.1; PID:g15457986; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C'Genetics:
A;Gene: PTS-EII
C;Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-534 «KUR»
A)Cross-references: UNIFROT: Q97XY4; GB:AE006641; NID:g13814802; PIDN:AAK41784.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein norB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A99316
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                             Length 440;
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                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred. No. 8.9;
7; Mismatches
                                                                                                                            7; Mismatches
                                                                                                                                                                                                                        3 LNTTV --- WPTIITPILLTLFLIT --- NRLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 10, 2004, 13:40:36
                                             Score 54;
Pred. No.
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                                         36.0%;
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Best Local Similarity 40.6
Matches 13; Conservative
                                                                                                                                     13; Conservative
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Best Local Similarity
Matches 7; Conserv
                                             Query Match
Best Local Similarity
Matches 13; Conserv
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A;Molecule type: DNA
A;Residues: 1-441 <KUR>
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A99316
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03.4ug-2001 #sequence_revision 03.4ug-2001 #text_change 09-Jul-2004
C;Accession: H95054
B;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.S.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClC A;Acference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D97155 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-395 <KUR>
A;Residues: 1-395 <KUR>
A;Cross-references: UNIPROT:Q97HEO; GB:AE001437; PIDN:AAK80031.1; PID:g15025060; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-440 <KUR>
A;Residues: 1-440 <KUR>
A;Cross-references: UNIPROT: Q97SB2; GB:AE005672; PIDN:AAK74633.1; PID:g14971945; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                          A;Genetic code: SGC1
C;Supertfamily: H+-transporting ATP synthase protein 8
C;Seywords: ATP biosynthesis; blocked amino end; hydrolase; membrane-associated complex;
F;I/Wodified site: blocked amino end (Wet) (probably formylated) #status experimental
A;Title: Identification of the subunits of F-IF-0-ATPase from bovine heart mitochondria.
A;Reference number: A39566; MUID:91242449; PMID:1827992
A;Accession: D39566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stage IV sporulation protein B, SpoIVB [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C; Accession: D97155 R; Nolling, J.; Brecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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C;Superfamily: Bacillus subtilis stage IV sporulation protein spoIVB
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Length 395;

DB 2;

36.0%; Score 54; DB llarity 47.4%; Pred. No. 8; Conservative 7; Mismatches

Query Match Best Local Similarity

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Matches

8 g

Molecule type: DNA

30

RESULT 13 H95054

11 IITPILLTLFLITNRLITT 29 |:||::| |:||:| 12 ILTPVILVVFLAYNKVIST

Indels

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A;Gene: SP0474
C;Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend
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A;Status: preliminary A; Molecule type: DNA

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RESULT 1
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Gérnza homo sapien
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 LRLNTTVWPTIITFILLTLFLITNRLITTR 30
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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sapı	homod	Aan14727	AAN14727	N	68	68.3	102.5	45
		Aan14716	AAN14716	7	68	68.3	102.5	44
		Aan14705	AAN14705	N	68	68.3	102.5	43
sapi		Aan14694	AAN14694	N	68	68.3	102.5	42
		Aan14683	AAN14683	7	68	68.3	102.5	41
		Aan14672	AAN14672	~	9	68.3	102.5	40
		Aan14661	AAN14661	~	9	68.3	102.5	39
		Aan14650	AAN14650	~	68	68.3	102.5	38
		Aan14639	AAN14639	~	9	68.3	102.5	37
		Aan14628	AAN14628	N	68	68.3	102.5	36
sapi	homo	Aan14617	AAN14617	0	68	68.3	102.5	35
		Aan14606	AAN14606	0	68	68.3	102.5	34
	homon	Aan14595	AAN14595	N	89	68.3	102.5	33
••	Omor.	Aan14584	AAN14584	7	89	68.3	102.5	32

ALIGNMENTS

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AY339446
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Irwin J.A., Parsons T.J.,
"Single nucleotide polymorphisms over the entire mtDNA genome that
"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.",
[1]
VARIANTS PRO.118:137-146(2004).
[7]
WARIANTS PRO.17 AND SER-21.
WABDLINE=92098084; PubMed=1757091;
MATZUKI S., Noer A.S., Lertrit P., Thyagarajan D., Kapsa R.,
Utthanaphol P., Byrne E.,
"Normal variants of human mitochondrial DNA and translation products:
the building of a reference data base.";
Hum. Genet. 88:139-145(1991).
                                                                                                                                                                                                                                                                                                                                                                              genome.";
Nucleic Acids Res. 26:967-973(1998).
-!- FUNCTION: This is one of the chains of the nonenzymatic component
- (CF(0) subunit) of the mitcohondrial Afrase complex.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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VARIANT THR-28.
MEDLINE-98127994; PubMed-9461455,
MEDLINE-98127994; PubMed-9461455,
Mieder M.J., Taylor S.L., Tobe V.O., Nickerson D.A.;
"Automating the identification of DNA variations using quality-based fluorescence re-sequencing: analysis of the human mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the ATPase protein 8 family.
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AAP89274.1;
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AY339420;
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